```
NON TER
SEQUENCE
                                                                                                                                                                                                                         Q95UA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                            Q95UA7
                                                        qq
                                                                                                            g
                                                                                                                                                                                                                                     셤
                                                                                    \delta
                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                          61 VITIESKGVQCESRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                       121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                         181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aeguorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M., Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aeguorea macrodactyla.
Bukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aeguoreidae; Aeguorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                        Ouery Match 83.7%; Score 1059; DB 5; Length 238; Best Local Similarity 80.7%; Pred. No. 3.4e-83; Matches 192; Conservative 18; Mismatches 28; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
83.6%; Score 1057; DB 5; Length 238;
Best Local Similarity 81.5%; Pred. No. Se-83;
Matches 194; Conservative 15; Mismatches 29; Indels
                                                                              Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF435430; AAL33915.1; -..
EMBL, AF435430; Penergy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IRR000786; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435432; AAL33917.1; -.
GO; GO:00066091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IRR00798; Green_fl_protein.
Pf01353; GFP; 1.
                                                                                                                                                     PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 27002 MW; BD5BA2982264C018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO1229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 27018 MW; 75521EA5534E573A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25, 0range fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                      macrodactyla.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           macrodactyla."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=OFPxm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBWTC5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
셤
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                qq
```

9

1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL

ò

```
121 NRIELKGMDFKEDGNILGHKLEYNFNSHNVYIMPDKANNGLKVNFKIRHNIEGGGVQLAD 180
                                                                           61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                          121 NRIELKGIDFKEDGNILGHKLEYNPISHNYYITADKOKNGIKANFKIRHNIEDGSVOLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 CFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGID 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 FKEDGNILGHK-LEYNFISHNVYITADKOKNGI------KANPKIRHNI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 EDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITH 231
                                                                                                                                                                                                                                                                             181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                          11 VVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKF-ICTTGKLPVPWPTLVTTFSXGVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||: |:: ::|
---VVLPEYHFV-----LSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q95UA7;
Q1-DRC-2001 (TrEMBLrel. 19, Created)
01-DRC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cyan fluorescent protein (Fragment).
Cyan fluorescent protein (Fragment).
Bukaryots, Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia; Paviina; Faviidae; Montastraea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 247.5; DB 5; Length 225; 
; Pred. No. 2.4e-13; 
46; Mismatches 71; Indels 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Falkowski P.G., Sun Y.;
FMANOMSTAREA CAVETHORS fluorescent protein.";
Whontastraea cavernosa fluorescent protein.";
Submitted (SEP-2001) to the EMBL/Genbank/DDBJ databases.
EMBL, AY056460; AAL17905.1;
EMBL, AY0564601; Penergy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR009017; GFP like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 AA; 25775 MW; 52DE2F716D083524 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   completed: April 19, 2004, 15:07:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.6%;
25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 GMD----ELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 DKDYNTVEVÝE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: A Job time: 46 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 KKG
```

à g  $\delta$ 셤 à g  $\stackrel{>}{\circ}$ Db

```
NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VITLGYGIQCFAKYPEHMKMNDFFKSAMPEGYIQERTIFFQDDGKYKTRGEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NRIELKGMDFKEDGNILGHKLEYNFNSHNVYIMPDKANNGLKVNFKIRHNIEGGGVQLAD 180
                                                                                                                                                               181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                   HYQTNVPLGDGPVLIPINHYLSFQTAISKDRNETRDHMVFLEFFSACGHTHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSKGEELFTGIVPVLIELDGDVHGHKFSVRGEGEGDADYGKLEIKFICTTGKLPVPMPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aequorea macrodactyla.
Bukaryota; Mecazoa, Cnidaria, Hydrozoa, Hydroida, Leptomedusae,
Aequoreidae, Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Li S.J., Xia N.S.; "Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 83.9%; Score 1061; DB 5; Length 238; Local Similarity 80.7%; Pred. No. 2.3e-83; les 192; Conservative 18; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          macrodactyla..;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AF495-428, AAL33913.1;
GO; GO:0006091; P:energy pathways; IEA.
InterPro: IPR009017; GFP like.
InterPro: IPR00917; GFP like.
Fine FPP (FPP) (FPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 AA; 27031 MW; 5F80A19C19DC584D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl_pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aequorea macrodactyla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=GFPxm162;
                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBWTC7;
                                                                                                                                                                                                                                                                                                                                                                                                   Q8WTC9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8WTC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
Q8WTC7
                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                   SO OR REPARED BY SO OR S
                                                                                     g
                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTIV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VITLGYGIQCFARYPEHMKMNDFFKSAMPEGYIQERTIFFQDDGKYKTRGEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aequorea macrodactyla.
Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=GFPxm163;
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                        Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 28; Indels
macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; PAF435429; PAL33914.1;
GO, GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR00786; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 27047 WW; 5F80A18FA1E7C84D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
83.9%; Score 1061; DB 5; 1
Best Local Similarity 80.7%; Pred. No. 2.3e-83;
Matches 192; Conservative 18; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                                              84.0%; Score 1062; DB 5;
80.7%; Pred. No. 1.9e-83;
ive 18; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 20, C (TrEMBLrel. 20, L (TrEMBLrel. 25, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                              Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBWTC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
```

DDT REPRESENTED THE PROPERTY OF THE PROPERTY O

셤

ठ

Db

ð

ö

9

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                            61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                   61 VITESYGIQCFARYPEHMKANDFFKSAMPEGYIQERIIFFQDDGKYKTRGEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                           121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                       VTIFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VITLSYGIÇCFARYPEHMKANDFFKSAMPEGYIQERIIFFQDDGKYKTRGEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRIBLKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                          HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                  181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guan B.Q., Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aequorea macrodactyla.
Bukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                      Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Li S.J., Xia N.S.; "Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.5%; Pred. No. 2.6e-84;
Matches 194; Conservative 18; Mismatches 26; Indels
                                                                                                          25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF435431; AAL33916.1; -.
GG), GG-0006091; Penerey pathways; IEA.
INTERPROPER TREAMMENT OF THE TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterProj issuigep, 1.
Prem, Prolass; GFP, 1.
PRINTS; PRO1229; GFLUGRESCENT.
ProDom; PD013756; Green_fl_protein; 1.
ProDom; P013756; Green_fl_protein; 1.
ProDom; P013756; Green_fl_protein; 1.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 27049 MW; 8185D0E55529012B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                              85.2%; Score 1078; DB 5;
81.9%; Pred. No. 7.8e-85;
ive 18; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                 Best Local Similarity 81.9%
Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A STRAIN=GFPxm19uv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       macrodactyla.";
                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBWTC6;
QBWTC6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
Q8WTC6
      SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                               ð
                                                                                                                                                                           Q
                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
61 VTLGYGILCFARYPEHMKMNDFFKSAMPEGYIQERTIFFQDDGKYKTRGEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSKGEELFTGVVPILVELDGDVHGHKFSVRGBGBGDADYGKLEIKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                  STRAIN=ShG24;
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                          Aequorea macrodactyla.
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=GRPxml61;
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia N.S.;
"Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF435433; AAL3918.1; -.
EMBL, AF435433; AAL3918.1; -.
EO,0006091; P:energy pathways; IEA.
InterPro; IPR009071; GFP like.
InterPro; IPR000786; Green fl_protein.
Pfam; PF01353; GFP, 1.
PRINTS; PR01229; GFLUCRESCENT.
PRODM: PD013756; Green fl_protein; 1.
SEQUENCE 238 AA; 26956 MW; 75521EAF0CEBA73A CRC64;
                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.1%; Score 1064; DB 5;
81.9%; Pred. No. 1.2e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Mismatches
                                              238
                                                                                      Created)
                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 20, (TrEMBLrel. 20, (TremBLrel. 25,
                                                                                    (TrEMBLrel. 20,
                                                                                                                                                  Green fluorescent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green fluorescent protein.
                                            PRELIMINARY;
                                                                                                            (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                       Aequoreidae; Aequorea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                        NCBI TaxID=147615;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       macrodactyla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002
01-MAR-2002
01-OCT-2003
                                                                                    01-MAR-2002
                                                                                                      01-MAR-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                          Q8WTC4
Q8WTC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8WTD0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBWTD0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
Q8WTD0
RESULT 9
                        OBWTC.
```

ö

```
NCBI_TaxID=6100;
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFPXM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
Q8WP95
                g
                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                             \dot{\delta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                       o;
                                                                           VTTPSXGVQCFSRYPDHMKRHDFFKKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                        61 VITEGYGYÇCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGGTLV 120
                                                                                                                   NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                           HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                       HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VITESXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                 Aequorea victoria (Jellyfish).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=6100;
                       °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 238;
Pred. No. 1.1e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
                                                                                                                                                                                                                                                                                                                                             [1] — SEQUENCE FROM N.A. Matching J.K.; BADL/GenBank/DDBJ databases. Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases. EMBL; X83959; CAAS8789.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 238 - 238 - 26950 MW; 26E2BE450E748E44 CRC64;
                                                                                                                                                                                                                              017105 PRELIMINARY, PRT; 238 AA.
017105;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.2%; Score 1192; DB 5;
92.9%; Pred. No. 1.2e-94;
live 7; Mismatches 10;
                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 AA
                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P42212; IGFL.

GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR000017; GFP like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PP01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
         96.2%;
       al Similarity 96.2
229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similaricy .... les 221; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                            181
                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
        Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
Q17106
ID Q17106
                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                     P
                                                                                             ДD
                                                                          ò
                                                                                                                                    qq
                                                                                                                  ð
                                                                                                                                                         à
                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \stackrel{>}{\circ}
```

```
61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VITFSYGVQCFSRYPDHMKQHDFLKSAMPEGYVQERIIFYKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRIELKGIDFKEDGNILGHKLEYNPISHNVYITADKQKNGIKANPKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NRIELKGIDFKEDGNILGHKWEYNYNSHNVYIMGDKFKNGIKVNFKIRHNIKDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKGEELFTGVVPILVELDGDVNGQKFSVRGEGEGDATYGKLTLKFICTTGKLDVPWPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 HYQQNTPIGDGPVLLPDNHYLSTQSALSQDPHGKRDHWVLLEFVTSAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-GFPAm, and GFPdnaxm,
STRAIN-GFPAm, and GFPdnaxm,
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,
Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.Q.,
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AV013824; AAK02062.1; -.
EMBL, AV013824; AAK02069.1; -.
GO, GO.0006091; Psencergy pathways; IEA.
InterPro; IPR009017, GFP Like.
InterPro; IPR009018; Green_fl_protein.
Fear, PF01353, GFP, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                               Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.4%; Score 1181; DB 5; Length 238; 92.4%; Pred. No. 1e-93; ive 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Watkins J.M., Campbell A.K.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X83960; CAA58790.1; -.
PIR; JS0662; JQ1514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 238 AA; 26867 MW; BD4648262D8EABD4 CRC64;
Q17106;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AA
                                                                                                                                                                                                                                                                                                                                                            HSSP, P42212; IBFP.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01353, GFP, 1.
PRINTS; PR01229, GFLUORESCENT.
ProDom; PD013756; Green fl_protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8WP95
Q8WP95,
Q8WP95,
Q8WP95,
Q1-MAR-2002 (TrEMBLrel. 20, Cx
Q1-MAR-2003 (TrEMBLrel. 20, La
Q1-OCT-2003 (TrEMBLrel. 25, La
Green fluorescent protein.
                                                                                                                                          Aequorea victoria (Jellyfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01229; GFLUORESCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 92.49
Matches 220; Conservative
                                                                                                                                                             Eukaryota; Metazoa; Cn
Aequoreidae; Aequorea.
```

ö

```
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6100
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (
01-FEB-1997 (
01-OCT-2003 (
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      093125
                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
Q93125
     à
                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                 유
                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VTTRSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVOLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                     NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVOLAD 180
                                          NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                181 HYOONTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                             181 HYQQNTPIGGGFVLLPDNHYLSTQSALSKDPNEKRDHWVLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 HYQQNTFIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                          Koranyi P., Berenyi M., Burg K.; "Occurrence of green fluorescence protein in diazotrophic bacteria Azomonas and Azotobacter."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                          Azomonas agilis.
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
NCBI TaxID=354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.5%; Score 1233; DB 2; Length 238; Best Local Similarity 97.1%; Pred. No. 3.5e-98; Matches 231; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26902 MW; 15FE9B9C5B4F6B89 CRC64;
                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                               238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 AA
                                                                                                                                                                                                                                                                                                                                    EMBL; AF324405; AAN86137.1; --
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Green fluorescence protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                Pseudomonadaceae; Azomonas.
NCBI_TaxID=116849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Green fluorescence protein.
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Azotobacter vinelandii.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                     121
                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                             Q8GHE4
Q8GHE4;
                                                                                                                                                                                                                375GFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8GHE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85GFP
                                                                                                                      RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
                                                                                                                                  28GHE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8GHE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                         ద
                                                                ò
                                                                                                                                               Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVOLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLTFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
Koranyi P., Berenyi M., Burg K.;
"Occurrence of green fluorescence protein in diazotrophic bacteria
Azomonas and Azotobacter.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF324406; AAN86138.1; -.
EMBL, AF324406; Penergy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR000917; GFP_like.
InterPro; IPR0009186; Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILINE=96505137; PubMed=8707053;
Cornack B.P., Valdivia R.H., Falkow S.;
"FACS-optimized mutants of the green fluorescent protein (GFP).";
Gene 173:33-38(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
COTMACK B.P., Betrram G., Egerton M., Gow N.A.R., Falkow S.,
Brown A.J.P.;
Brown A.J.P.;
Weast Enhanced Green Fluorescent Protein (yEGFP): a reporter of expression in Candida albicans.";
Microbiology 0:0-0(1996).
Microbiology 0:0-0(1996).
EMBL, U73901; AABL8957.1; -.
HSSP; P42212; 1BFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.0%; Score 1227; DB 5; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 238 AA; 26887 MW; E0E1616BD2AF6188 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incerto, Annocastic Pression Pression Programs, Prosson Prosson Prosson Prosson Prosson, Prosson, Prosson, Prosson, Prosson, Prosson, Prosson Prosson, Prosson Prosso Prosson 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.4%; Score 1232; DB 2; 97.1%; Pred. No. 4.3e-98; iive 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Green fluorescent protein mutant 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aequorea victoria (Jellyfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 97.1
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
```

1

```
April 19, 2004, 15:02:40; Search time 45 Seconds (without alignments) 1668.741 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                  US-10-057-505-2-COPY
1265
1 MSKGEELFTGVVPILVELDG......VLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                              1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unclassified: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sp archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
Sequence:
                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                               Searched:
                                                                             Run on:
```

		Description	ORdhel azotobacter	370000000		Ogalos asomores asi		Q1/105 aequoted Vi						Q8wtc8 aeguorea ma	O8wtc9 aequorea ma				Orough montactraca	
SUMMAKIES		ID	Q8GHE2	O8GHE4	O8GHE3	093125	017105	017106	26dM80	S WILL	D8WTC4	TO THE OCCUPANT OF THE OCCUPAN		Cawarca	Q8WTC9	OBWIC7	OBWTC5	741120	0720WS	
		DB	7	~	~	Ŋ	Ŋ	'n	S	ĸ	ı	u	) U	n	'n	Ŋ	ιΛ	ď	'n	
		Match Length DB	238	238	238	238	238	238	238	238	238	α 3 C	0 0	239	238	238	238	225	225	
٩	* Query	Match	97.9	97.5	97.4	97.0	94.2	93.4	85.2	84.7	84.1	84	0		83.5	83.7	83.6	19.6	19.6	
		Score	1238	1233	1232	1227	1192	1181	1078	1072	1064	1062	1061	1 6	1961	1059	1057	247.5	247.5	
	Result	No.	1	7	m	4	S	φ	7	80	σ	10		1 6	71	13	14	15	16	

Q720w9 montastraea Q963f5 montaetraea Q8i6j8 trachyphyll Q8mu48 montaetraea		anemonia scolymia meandrina mentastra montastra discosoma montastra	Q81512 montastraea Q9gpi5 anemnia su Q95vt0 montastraea Q816C9 radianthus Q9b179 renilla mue Q9u6y7 anemonia su Q7z168 cerianthus Q8isf8 parasicyoni
Q7Z0W9 Q963F5 Q816J8 Q8MU48 Q8T5F1	0906Y3 0720W4 08T6U0 08MMA2 0720W6	0916x6 0815x0 086LV7 096LV8 090W4 0906x8 0962P9 0760W8	Q01557 Q045VT0 Q85VT0 Q816T9 Q916Y7 Q9GZ28 Q7Z168
លសហសស	. ល <b>ល ល ល ល</b> ល	սոսոսոսոսու	առաառաառա
225 225 225 225 225	255 255 253 253 253	222 234 234 225 227 227	232 232 233 232 232 232 231
1.81 1.81 1.81 1.00	000000	1166.2 1166.2 1166.2 1166.2 1166.3 11	
241.5 239.5 236.5 229 228	225.8 225.5 224.5 208.5 208	2005.5 2002.5 2002.5 2002.5 1999.5 1999.5	196.5 198.5 198.5 198.5 199.5 189
17 18 19 20 21	22 23 24 26 27 60	2 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	) W W 4 4 4 4 4 8 0 0 0 11 01 W 4 N

#### ALIGNMENTS

																												Ö	09	09
															, c	<b>5</b>												Gaps	MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL	MSKGEELFTGVVPILVELDGDVNGHKFSVSGGGGGDATYGKLTKFICTTGKLPVFWPTL
									2						T P T													. 0	KLPV	KLPVI
								, הקיים	5						, d	}										238;	•	m	CITIC	
								domo							roph	4	9868	}							64;	Length 238;	)	Indels	TLKF	TLKF)
			(e)	date)				Paet	1						azot		latab								CRC				YGKL	ZĞE
	ď.		updat	n upo	•			ria:	,						in di		DBJ C	,							64018	OB 2;	3-98;	N.	SGDAT	GDAT
	238 AA.		sequence update)	Last annotation update)				Bacteria; Proteobacteria; Gammaproteobacteria: Pseudomonadales							"Occurrence of green fluorescence protein in diazotrophic bacteria		Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases		:						238 AA; 26914 MW; F84840F1F9064018 CRC64;	Score 1238; DB 2;	Pred. No. 1.3e-98;	cheв	SGEGI	SGEG
		ed)	sedne	annot				oteok							prot	•	JenBa		IEA		cein.			1; 1.	1840F	123	No.	ismat	IKFSV	IKFSV
	PRT;	Created)	Last	aBt				mapr						Χ	ence		MBL/		Ways	InterPro; IPR009017; GFP like.	InterPro; IPR000786; Green fl protein.	<b>\</b>	٠.	otei	£8.	Score	Pred	1; Mismatches	DVNG	DANG
		23, (	23, I					: Gan	Pseudomonadaceae; Azotobacter.					Koranyi P., Berenyi M., Burg K.;	oresc	 -	the E	EMBL; AF324408; AANB6140.1;	path	like	en fl	í	PRINTS; PR01229; GFLUORESCENT.	fl pr	4 MW;			-	ÆLDG	TAETDG
	PRELIMINARY;	:e1.		el.	rote		lii.	eria	otob					Σ	flu	cter	ţ	6140	ergy	GFP	Gre	1.	UORE	een_	2691	97.98;	97.5%;	tive	VPIL	VPIL
	LIMIN	(TrEMBLrel.	(TrEMBLrel.	(TrEMBLrel.	uce I		eland	pact	3; Az			Ä		enyi	green	toba	2000)	AANB	P:en	3017;	786;	3FP;	GFL	S; Gr	\$		ty.	erva	FTGV	FTGV
	PRE			(Tr	eace		vin	rote	acea	354;		N WO	289;	Ber	of	d Azd	NOV-	408;	160	PROOS	PR00(	53; (	1229	13756	238 7		ilari	Con	KGEEL	KGEEI
		01-MAR-2003	01-MAR-2003	01-OCT-2003	Green fluorescence protein.	۰:	Azotobacter vinelandii.	ia; P	nonad	NCBI TaxID=354;		SEQUENCE FROM N.A.	STRAIN=DSM2289;	Ъ.	ence	Azomonas and Azotobacter.";	) pa:	AF324	9000	н 6	0; I	Pfam; PF01353; GFP; 1.	PR0	PD0	Ħ	ť	Sim.	232; Conservative	1 MS	ר א MS]
1	Q8GHE2	-MAR	-MAR	-OCT	een 1	2289GFP.	otoba	cter	eudor	BI Te		QUENC	RAIN:	rany	ccuri	ополе	bmitt	BL; 7	ë S	terPı	terPi	am; E	INTS	ProDom;	SEQUENCE	Matc	Local			
RESULT OBGHE2	88	01	0.1	01	g	22	Az	Ba	PB	N	ᅼ	SE	ST	8	Õ	Az	Su	Ä	8	ä	H	PÉ	PR	Pr	SE	Query Match	Best Local Similarity	Matches		
RES OBC	A D	Į	DI	L	DE	Z	os	ပ္ပ	ပ္ပ	ŏ	KN	RP	RC	R.A	RT	RI	RL	DR	DR	DR	DR	DR	DR	DR	Š	a	DO)	Σ	ò	qq

o,

61 VTTESXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120

à

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

April 19, 2004, 15:04:50 ; Search time 22 Seconds (without alignments) 558.499 Million cell updates/sec

1265 1 MSKGEELFTGVVPILVELDG......VLLEFVTAAGITHGMDELXK 238 US-10-057-505-2-COPY Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 seqs, 51625971 residues Searched:

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued\_Patents AA:\*
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	40.0	י ביי	1000	ו המקלה רמת א	יותעע	יושמי	Applit	רממל	TAGE.	יי קיר מרא	י בשמע ע	11000	1144	450	Appli	Appli Appli	
ជ	100	, c	10	i	'n	7	7	ci.	H	2	74		,	, ,	3	· -	ì	, ,	7 1	;	, 4	,	٠ L		v c	, N	
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Semience	Semience	Seminary	Segmente	Segment	Segment	Segrence	Segment	Segrences	Segment	Segmente	2010100	Sequences.	Sognon	Sequence	Sequence	•
											•**								53				ư				
	08-753-143-2 08-679-866-2	-876	-553-	-144-	-094-359-2	172-06	263-975-	-727	-418	-129-192C-2	-129-192C-74	-602-641-2	-463-	-893-327-	-337-915A-2	-121-539-1	-214-909-2	-479-645A-1	-645A-1	-065A-4	US-09-920-922-4	PCT-US95-14692-2	"	-646-538-2	-503-222-2	-472-065A-2	
	US-08	0S-08	US-08	US-08	US-09-094	0S-09	50	Ö	0-SD	US-09	US-09-129	US-09-605	US-09	US-08-	US-08-337	US-09-121	US-09-214	-60-SD	US-09-479	US-09	US-09	PCT-U	US-09	IIS-08	-60-Sn	US-09	
DB	4 0	1 (1	7	ო	m	<b>г</b> О .	m ·	4.	4	4	4	4	4	m	Н	m	4	4	4	4	4	Ŋ	4	m	m	4	
Length	238	238	238	238	238	238	238	277	73B	238	238	238	238	247	238	238	238	238	238	238	238	238	238	239	239	238	
% Query Match	97.9	97.9	97.9	97.9	97.9	97.9	y .	2.10	y	97.9	97.9	97.9	97.9	97.8	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5			
Score	1238 1238	1238	1238	1238	1238	1238	1738	1170	1238	1238	1238	1238	1238	1237	1234	1234	1234	1234	1234	1234	1234	1234	1233	1233	1233	m	
Result No.	7 7	М	বা ।	ın v	.o I	<b>~</b> c	<b>10</b> 0	, ,	2 7	T ;	12	13	14	1.5	16	17	18	19	20	21	22	23	24	25	26	27	

Seguence 94, Appl	Sequence 96. April	Semience 98 April	100		Semience 104 ann		2 AT	ì	Semience 2 Annli		, c	10	Sequence 66, Appr	sednence 90, Appl	Sequence 92, Appl	Semience 148 Ann		
US-09-479-645A-94	US-09-479-645A-96	US-09-479-645A-98	US-09-479-645A-100	US-09-479-645A-102	US-09-479-645A-104	US-09-479-645A-110	US-09-091-042A-2	US-09-127-227-2	US-08-588-201-2	US-09-169-605-2	US-08-893-327-2	TIS-09-479-645b-88	11S-02-479 GARA	06-4640-614-60-00	US-09-479-645A-92	US-09-479-645A-148	US-09-479-645A-150	US-09-479-645A-152
4	4	4	4	4	4	4	4	4	7	N	m	4	٠ 4	۰,	4	4	4	4
243	243	243	243	243	243	243	1070	1452	238	238	238	243	243	2 6	243	243	243	243
97.3	97.3	97.3	97.3	97.3	97.3	97.3	97.3	97.3	97.2	97.2	97.2	97.2	97.2		7.16	97.2	97.2	97.2
1231	1231	1231	1231	1231	1231	1231	1231	1231	1230	1230	1230	1230	1230	1 1	1630	1230	1230	1230
28	53	30	31	32	33	34	35	36	37	38	39	40	41		7.	43	44	45

#### ALIGNMENTS

```
61 VITTESKGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFRGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                       61 VITFSYGVQCFSRXPDHWKRHDFFKSAMPEGYVQERIFFKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                                                                                                                                            121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                           181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                       Length 238;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tsien, Roger Y.
APPLICANT: Cubit, Andrew B.
TITLE OF INVENTION: Assays for Protein Kinases Using
TITLE OF INVENTION: Fluorescent Protein Substrates
CORRESPONDENCE: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   Query Match
97.9%; Score 1238; DB 1;
Best Local Similarity 97.5%; Pred. No. 6.8e-127;
Matches 232; Conservative 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-679-865-2; Sequence 2, Application US/08679865; Patent No. 5912137; GENERAL INFORMATION:
                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Aequorea victoria
US-08-753-143-2
                                                                                                                                                              SEQ ID NO 2
LENGTH: 238
                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

ô

```
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: La
STATE: Ca
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-792-553-2
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NRIBLKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
97.9%; Score 1238; DB 2; Length 238;
Best Local Similarity 97.5%; Pred. No. 6.8e-127;
Matches 232; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cubitt, Andrew B.
TILLE OF INVENTION: Assays for Protein Kinases Using
TITLE OF INVENTION: Assays for Protein Substrates
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                      COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,865
FILING DATE: 16-UUL-1996
CLASSIFICATION: 435
ATTORNEY/ACCITATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 941113834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
ADDRESSEE: Townsend and Townsend and Crew LLP
STRET: Two Enbarcadero Center, Eighth Floor
STRIE: San Francisco
STRIE: California
                                                                                                                                                                                                                                                                                                                                                           02307Z-069000
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Storella, John S.
REGISTRATION NUMBER: 32,94
REFRENCE/DOCKET NUMBER: 02307
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAK: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08680876
Patent No. 5925558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 238 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-679-865-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                          COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-680-876-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIFHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NRIBLKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTIGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.9%; Score 1238; DB 2; Length 238; 97.5%; Pred. No. 6.8e-127; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08792553
Patent No. 5981200
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Heim, Roger
TITLE OF INVENTION: Tandem Fluorescent Protein Constructs
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,553
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/POCKET NUMBER: 07257/041001/UC 96-160-2
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07257/041001/UC 96-160-2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,876
FILING DATE: 16-UUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John S.
REGISTATION NUMBER: 32,944
REPRENCE/DOCKET NUMBER: 02307Z-0692
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92037
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                           ...: 2
.....TERISTICS:
TYPE: amino acid
TOPOLOGY: 1:---
OLECTH
                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 97.5
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-680-876-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   La Jolla
: California
RY: USA
```

```
97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 97.5%;
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 238
TYPE: PRT
ORGANISM: Aequorea victoria
                                          Query Match
Best Local Similarity 97.5
Matches 232; Conservative
        US-08-753-144-2
                                                                                                                                                                                                                                                                                                                                                                                                               US-09-094-359-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-094-359-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-172-063-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
                                                                                                                                          d
                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                   61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                            121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                        181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                             1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                   1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                          Gaps
                                                                                                                                                        .;
0
                                                                                                                       Length 238;
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08753144

Patent No. 6066476
GENERAL INFORMATION:
APPLICANT: Heim, Roger
TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                     Score 1238; DB 2;
Pred. No. 6.8e-127;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windiws95
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,144
FILING DATE: 20-NOV-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla STREET CA COMMENTE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/727,452
FILING DATE: 10-0CT-1996
APPLICATION NUMBER: 0855/14692
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: 0855/14692
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFRENCE/DOCKET NUMBER: 07257/032002
TELECOMMUNICATION INFORMATION:
                                                                                                                     97.9%;
               : 238 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 amino acids
mino acid
                                                                                                                                 Best Local Similarity 97.5
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTAL
ZIP: 92037
COMPUTER READABLE FORM:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS LENGTH: 238 amino acid TYPE: amino acid TOPOLOGY: linear
                            TYPE: amino acid
TYPE: amino acid
TYPE/OGY: linear
MOLECULE TYPE: protein
US-08-792-553-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -08-753-144-2
                                                                                                                 Query Match
                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                      Db
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                61 VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                61 VITESYGVQCFSRYPDHMKRHDFFKSAMPBGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                  121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                       181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                      181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMV1LEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                              1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLDVPWPTL
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09094359;
Patent No. 6140132;
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Llopis, Juan
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/067001
CURRENT APPLICATION NUMBER: US/09/094,359;
CURRENT FILING DATE: 1998-06-09;
NUMBER OF SEQ ID NOS: 18
     Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 238;
                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
Score 1238; DB 3;
Pred. No. 6.8e-127;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1238; DB 3;
Pred. No. 6.8e-127;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/09172063
; Patent No. 6150176
; GENERAL INFORMATION:
; APPLICANT TRien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Llopis, Juan
```

```
TELEFAX: (415) 576-0300 INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 238 antino acids.
                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                US-09-263-975-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-08-727-452-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                       TYPE:
                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VITESYGVÇCESRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NRIELKGIDFKEDGNILGHKLEYNYNSHNYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                             09
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                      ;
0
          APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/172,063
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 09/094,359
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASELSEQ for Windows Version 4.0
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                          Score 1238; DB 3; Length 238;
Pred. No. 6.8e-127;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09263975
Patent No. 6248550
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Assays for Protein Kinases Using TITLE OF INVENTION: Fluorescent Protein Substrates NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/679,865
FILING DATE: 16-UL1-1996
ATORNEY/AGENT INFORMATION:
NAME: Storella, John S.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 02307Z-069000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                        tch
al Similarity 97.5%;
232; Conservative 1
APPLICANT: Wachter, Rebekka M.
                                                                                                                                                                                                                                                                         ; ORGANISM: Aequorea victoria
US-09-172-063-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-09-263-975-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                             61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                 61 VITESYGVQCFSRXPDHMKRHDFFKSAMPEGYVQERTIFFKDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NRIELKGIDFKEDGNILGHKLEYNFISHNYYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VITESXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRABVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VITESYGVQCFSRXPDHAKKHDFFKSAMPEGYVQERIIFPKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVOLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Telen, Roger Y.
APPLICANT: Telen, Roger Y.
APPLICANT: Telen, Roger
TITLE OF INVENTION: FLUCRESCENT PROTEIN SENSORS FOR DETECTION OF ANALYTES
TITLE OF INVENTION: FLUCRESCENT PROTEIN SENSORS FOR DETECTION OF ANALYTES
CURRENT APPLICATION NUMBER: US/08/727, 452A
CURRENT FILING DATE: 1996-63-20
EARLIER PILING DATE: 1995-11-13
EARLIER PLILNG DATE: 1995-11-13
EARLIER PILING DATE: 1994-11-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FREEEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                    .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.9%; Score 1238; DB 4; Length 238; Best Local Similarity 97.5%; Pred. No. 6.8e-127; Matches 232; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                           Score 1238; DB 3;
Pred. No. 6.8e-127;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08727452A
Patent No. 6319669
                                                                                                                                                           97.9%;
238 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Aequorea victoria
US-08-727-452-2
                                                                                                                                                      Query Match
Best Local Similarity 97.5
Matches 232; Conservative
                                             TOPOLOGY: linear
MOLECULE TYPE: protein
```

S

ö

9

```
Sequence 74, Application US/09129192C

Patent No. 649564

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Autorea Biosciences Corporation
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
FILE REPERENCE: AUROL700 (098366/031001)
CURRENT APPLICATION NUMBER: US/09/129,192C

UNRENT FILING DATE: 1998-07-24

NUMBER OF SEQ ID NOS: 74

SOFTWARE: Patentin version 3.0

SEQ ID NO 74
                                                                                                                             61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                            121 NRIELKGIDFKEDGNILGHKLEYNFISHNYYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VTTFSYGVQCFSRXPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGGDATYGKLTLKFICTTGKLDVPWPTL 60
                                                                                                                                                                                                                                                                                                                  181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                          181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Aequorea green fluorescent protein phosphorylation mutant
US-09-129-192C-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Llopis, Juan
APPLICANT: Recekka M.
APPLICANT: Remington, S. James
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.9%; Score 1238; DB 4;
97.5%; Pred. No. 6.8e-127;
cive 1; Mismatches 5;
  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/09/602,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/09602641; Patent No. 6608189; GENERAL INFORMATION:
232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-129-192C-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-602-641-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Matches
                                                                                                                                ò
                                                                                                                                                                           g
                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \stackrel{>}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Auora Biosciences Corporation
APPLICANT: Auora Biosciences Corporation
APPLICANT: Cubitt, Andrew B.
TITE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
FILE REFERENCE: AUROL270 (08366/031001)
CURRENT APPLICATION NUMBER: US/09/129,192C
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.0
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VITESXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIJFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTKFICTIGKLFVPWPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                          APPLICANT: Fisher, Hugh
TITLE OF INVENTION: Rapidly Greening, Low Oxygen Mutant of
TITLE OF INVENTION: Rapidly Greening, Low Oxygen Mutant of
TITLE OF INVENTION: the Aequorea victoria Green Fluorescent Protein
FILE REFERENCE: RAC 99-0011
CURRENT APPLICATION NUMBER: US/09/418,785
CURRENT APPLICATION NUMBER: 099-10-15
PRIOR APPLICATION NUMBER: 60/104,563
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1238; DB 4; Length 238; Pred. No. 6.8e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 238;
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Aequorea victoria
PUBLICATION INFORMATION:
AUTHORS: Prasher, D.C. et al.
TITLE: Primary structure of the Aequorea victorea green-f
VOLUME: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.9%; Score 1238; DB 4;
97.5%; Pred. No. 6.8e-127;
ative 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAGES: 229-233
DATE: 1992-01-01
DATABASE ACCESSION NUMBER: Genbank M62653
DATABASE ENTRY DATE: 1993-04-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09129192C Patent No. 6495664 GENERAL INFORMATION:
                                                    ; Sequence 1, Application US/09418785; Patent No. 6414119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Aequorea
US-09-129-192C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-129-192C-2
                            US-09-418-785-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-418-785-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
```

g

g à qq ò g

ŏ

· 0

181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                               61 VITPSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                   61 VITESYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NRIBLKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VITESYGVÇCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTIGKLFVPWPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 HYQQWTPIGDGPULLPDNHYLSTQSALSKDPKEKRDHWYLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                       1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                    1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Taien, Roger Y.

APPLICANT: Hipawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
APPLICANT: Mipawaki, Muan
TITLE OF INVENITON: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/067001
CURRENT APPLICATION NUMBER: US/09/704,463
CURRENT FILING DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 18
SOFFWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1238; DB 4; Length 238; Pred. No. 6.8e-127; 1; Mismatches 5; Indels
                                                                                                                                                                                                                             Length 238;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                     Query Match
97.9%; Score 1238; DB 4;
Best Local Similarity 97.5%; Pred. No. 6.8e-127;
Matches 232; Conservative 1; Mismatches 5;
                                                          NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 238
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/172,063
PRIOR FILING DATE: 1998-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09704463
Patent No. 6627449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.9%;
                                                                                                                                       ; TYPE: PRT
; ORGANISM: Aequorea victoria
US-09-602-641-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Aequorea victoria
US-09-704-463-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 97.5
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-704-463-2
                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRABVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 VITFSHGVQCFSRXPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFLCTTGKLPVPMPTL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITHGMDELYK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 247;
                                                                                              GENERAL INFORMATION:

APPLICANT: Zolotukhin, Sergei
APPLICANT: Hauswirth, William W.
APPLICANT: Muzyczka, Nicholas
TITLE OF INVENTION: Humanized Green Fluorescent Protein
TITLE OF INVENTION: Genes and Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZITE: TX
COUNTRY: USA
ZITE: 77210-4433
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
97.8%; Score 1237; DB 3;
Best Local Similarity 97.5%; Pred. No. 9.3e-127;
Matches 232; Conservative 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UFLA:062\KIT.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
INFORMATION POR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: April 19, 2004, 15:08:34 Job time : 23 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,201
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
                                                      Sequence 20, Application US/08893327
Patent No. 6020192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
HOLECULE TYPE: protein
US-08-893-327-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                     Houston
RESULT 15
US-08-893-327-20
```

us-10-057-505-2-copy.rag

100,

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

- protein search, using sw model OM protein April 19, 2004, 14:55:50 ; Search time 60 Seconds (without alignments) 1120.772 Million cell updates/sec Run on:

1265 1 MSKGEELFTGVVPILVELDG......VLLEFVTAAGITHGMDELYK 238 US-10-057-505-2-COPY Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* A Geneseq 29Jan04:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp2000s:\* .. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	TOOKY BOKKOWK	Ler 30035544	AA831878 GED	DATE BY STATE OF THE PARTY OF T	viler 900375044	Aah73554 Gree	Ada05013 Gree	SOLD CIEROMEN	2017 217721111
8	AAW05309	ABG76006	AAW31878	AAW31879	ABG76009	AAB73554	ADA25213	AAWOS310	
DB	. 2	9	2	~	ø	4	ø	~	
Query Match Length DB	238	238	501	501	238	238	238	238	1 1
Query Match	99.5	99.5	99.4	99.4	98.8	98.2	98.2	98.1	
Score	1259	1259	1257	1257	1250	1242	1242	1241	
Result No.	н	2	М	4	ιΩ	9	7	œ	(

		Descrip	Aawosane film	9		1879 GFD	م ،	٠ 4	3 Green	0	05 Jellvf	) H	88	G GFP	- م	6	17	86	4	08 Green	32	. A	יס	81 A	A	[ F. W.	,
		E C	AAW05309	ABG76006	AAW31878	AAW31879	ABG76009	AAB73554	ADA25213	AAW05310	ABG76005	AAE34991	AAW31880	AAW31876	AAB73553	AAE34992	AAW05311	AAE34998	AAW05304	AAW05308	AAW24232	AAW76105	AAW40479	AAW65081	AAW76371	AAB73552	
		DB :	7	9	2	7	9	4	ø	~	9	9	7	7	4	9	N	9	~	~	~	7	~	7	~	4	•
		Length	238	238	501	501	238	238	238	238	238	238	501	514	238	238	238	238	238	238	238	238	238	238	238	238	000
•	Query	Match	99.5	99.5		99.4		98.2		98.1			98.1		٠.	98.0		97.9				97.9					0
		Score	25	25	25	1257	25	24	24	24	24	4	24	24	24	1240	23	23	1238	23	1238	23	23	1238	23	33	ć
	14	.:	н	7	м	4	'n	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	п

Aequorea Aequorea Aequorea	Jellyfish Jellyfish Aequorea	Aequorea Wild-type Green flu Aequorea	GFP varia Aequorea A. victor A. victor	Green flu Green flu Aequorea	Vellyllsh Aequorea Humanised
Aae16056 Aae16038 Abg32365	Abg76012 Abg75980 Aae34999	Add 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Aaw31877 Aaw22100 Aaw65084 Aaw65082	Aay43248 Aab73555 Aae16057	Aaw96330 Aaw96330
AAE16056 AAE16038 ABG32365	ABG76012 ABG75980 AAE34999 AAE34003	ABR44423 ADA25219 ADA25194	AAW31877 AAW22100 AAW65084 AAW65082	AAY43248 AAB73555 AAE16057 ARG76013	AAE34990 AAW96330
ហហហ	νυνυ	999	0000	01 44 RD AC	1000
238 238 238	238 238 238	238 238 238 238	501 238 238 238	238 238 238	238
9.7.9 9.7.9	9.7.9 9.7.9 9.7.9	97.9 97.9 9.79	97.9 97.8 97.8	97.8 97.8 97.8	97.8
1238 1238 1238	1238 1238 1238	1238 1238 1238	1238 1237 1237 1237	1237 1237 1237	1237
26 27 28	33 31 31 31	E 4. E	9 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 0 11 5 6	44 45 45

#### ALIGNMENTS

AAW05309 standard; protein; 238 AA. (first entry) 02-APR-1997 AAW05309; RESULT 1 AAW05309 

Green fluorescent protein mutant Y66W/N146I/M153T/V163A/N212K.

Green fluorescent protein; GFP; jellyfish; Aequorea victoria; sea pansy; Renilla reniformis; differential gene expression; protein localisation; gene expression tracking; fluorescence.

Synthetic.

Location/Qualifiers /note= "V163A" 212 /note= "N212K" /note= "N146I" Misc-difference 153 /note= "M153T" /note= "Y66W" Misc-difference 146 Misc-difference 163 Misc-difference 66 Misc-difference WO9623810-A1.

88-AUG-1996

94US-00337915. 95WO-US014692 (REGC ) UNIV CALIFORNIA. 13-NOV-1995; 10-NOV-1994;

WPI; 1996-371370/37 Tsien RY, Heim R;

New modified Aequorea green fluorescent polypeptide(s) - having amino acid changes to provide prods. Which exhibit different excitation and emission spectra.

Claim 11; Page ?; 39pp; English.

96US-00594575. 97US-00792553. 99US-00396003.

31-JAN-1996; 31-JAN-1997; 13-SEP-1999;

25-JAN-2002; 2002US-00057505.

Cubitt A;

Tsien RY,

WPI; 2003-247255/24

(REGC ) UNIV CALIFORNIA. Heim R,

```
Direction (GFP) of the invention (see AAW0504 for the wild type protein).

The fluorescence of this protein is generated by cyclisation and confident of the Ser-Tyr-04/9 sequence at positions 65-67. Asquores GFP has two absorbance peaks, as opposed to the one absorbance peak seen in the sea pansy (Renilla reniformis). The modifications present in these sequences were created by subjecting the conditions present in these sequences were created by subjecting the CC DNA encoding this sequence to site directed mutagenesis using mutagenic CP PR primers, or hydroxylamine treatment. These GFPs of the invention are modified to lead to the formation of products with markedly different CC excitation and emission make these products with markedly different contexts, such as tracking of differential gene expression and protein contexts, such as tracking can also be created to modify the encoded GFP CS that it only possesses one absorbance peak
```

Sequence 238 AA;

```
ö
                                                                              VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                            NRIBLKGIDFKEDGNILGHKLEYNPISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                    9
                                           9
                                                                                                                                                                HYQQNTPIGDGPVLLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                          1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLILKFICTTGKLPVPWPTL
                      Gaps
                      ô
 Length 238;
                    1; Indels
Score 1259; DB 2;
Pred. No. 1.7e-122;
                    1; Mismatches
99.5%;
                 Matches 236; Conservative
        Local Similarity
                                                                                61
                                                                                                                       121
                                                                                                                                                                                   181
Query Match
                                                                                                                                                               181
                                       à
                                                         g
                                                                              ð
                                                                                              ΩD
                                                                                                                     \delta
                                                                                                                                        엄
                                                                                                                                                              à
                                                                                                                                                                                Db
```

ABG76006 standard; protein; 238 (first entry) Jellyfish GFP mutant W7. Aequorea victoria 30-APR-2003 ABG76006; 

Ā

fluorescent resonance energy transfer; tandem fluorescent protein; enzymatic assay; Alzheimer's disease; hypertension; inflammation; apoptosis; AlbS; acquired immunodeficiency syndrome; mutein. Jellyfish; enzyme; green fluorescent protein; GFP; FRET; mutant;

Synthetic.

'note= "Wild-type Tyr substituted by Trp" note= "Wild-type Asn substituted by Ile" /note= "Wild-type Asn substituted by /note= "Wild-type Met substituted by 'note= "Wild-type Val substituted by Location/Qualifiers Misc-difference 153 Misc-difference 163 Misc-difference Misc-difference Misc-difference

US2002164674-A1

Ŗ.

AAW31878 standard; protein; 501

03-FEB-1998 (first entry)

AAW31878;

HXXXH

07-NOV-2002.

```
comparising a donor or acceptor funcescent protein moiety (e.g. jellyfish green fluorescent protein, GPP) or a linker moiety that couples the donor and acceptor moieties. Also include are a recombinant nucleic acid coding for the tandem fluorescent protein construct, an expression of the tandem fluorescent protein construct, an expression control sequences operatively linked to a sequence coding for the expression of the tandem fluorescent protein construct, a host cell transfected with the expression vector. Getermining whether a sample contains an enzyme or whether a compound a lersy the activity of an enzyme, determining the amount of activity of an enzyme in a cell and testing for cleavage enzyme activity. The tandem fluorescent protein construct is useful in enzymatic assays, using the donor and acceptor moieties. The tandem fluorescent proteins are particularly useful in assays for protease activity. Proteases play an essential role in many disease processes e.g. Alzheimer's disease, hypertension, inflammation, apoptosis and AIDS (acquired immunodeficiency syndrome). Tandem fluorescent proteins were constructed comprising mutants of GFP with altered fluorescent spectra. The present sequence of shown in the specification but was created by the bindexer using the information in the specification and the wild-type GFP protein appearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VITFSWGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New tandem fluorescent protein construct comprising a donor or acceptor fluorescent protein moiety or a linker moiety that couples the donor and acceptor moieties, useful in enzymatic assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK
                                                                                                                                                                                                                                                                                                                                                                                           invention relates to a tandem fluorescent protein construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.5%; Score 1259; DB 6; Length 238; 99.2%; Pred. No. 1.7e-122; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                               Claim 3; Page; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 236; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          면
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \overset{\circ}{\sigma}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

m

```
GFP variants S65C and W7 tandem fluorescent protein construct.

North West Pacific jellyfish; green fluorescent protein; GFP; S65C;
fluorescent resonance energy transfer; FRET; enzymatic assay; W7;
enzyme inhibitor; enzyme promoter; PCR primer; protease cleavage site;
Tandem fluorescent protein construct; blue fluorescent protein.
```

Synthetic. Aeguorea victoria.

```
/note= "wild type Ser substituted with Cys" 239. .264
| Jabel= linker_moeity
                                                                                                                                                                                                                                                                                /note= "wild type Tyr substituted with Trp
                                                                                                                                                                                                                                                                                                                                                                                                                           Val substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= N212K
/note= "wild type Asn substituted with Lys"
                                                                                                                                                                                                                                                                                                                              'note= "wild type Asn substituted with Leu"
                                                                                                                                                                                                                                                                                                                                                                             Met substituted with Thr"
                                                                                                                                                                                 250. .251
/label= trypsin_cleavage_site
                                                                                                                                                                      calpain_cleavage_site

    .238
    label= S65C_GFP_variant

                                                                                                                                                                                                                165. .501 -- -- -- /label= W7_GFP_variant
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     /label= V163A
/note= "wild type"
                                                                                                                                                                                                                                                                                                                                                                           'note= "wild type
                                                                                                                                                                                                                                                                                                             label= N146L
                                                              /label= $65C
                                                                                                                                                                                                                                                                label= Y66W
                                                                                                                                                      253. .254
/label= ca
                                                                                                                                                                                                                                                                                                                                                             label=
                                            Misc-difference
                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                       Cleavage-site
                                                                                                                                                      Cleavage-site
                                                                                                                                                                                   Cleavage-site
                Protein
```

WO9728261-A1.

07-AUG-1997.

31-JAN-1997; 97WO-US001457

31-JAN-1996; 96US-00594575.

(REGC ) UNIV CALIFORNIA. (AURO-) AURORA BIOSCIENCES CORP

Isien RY, Heim R, Cubitt A;

WPI; 1997-402615/37.

Tandem fluorescent protein constructs - have donor and acceptor moieties exhibiting fluorescent linked via cleavable peptide linker, useful in exhibiting fluorescent linked via cleavable peptide linker, useful in Claim 3; Page; 88pp; English.

This protein sequence is that of a novel tandem fluorescent protein construct, made using Aequorea victoria (North West Pacific jellyfish) green fluorescent protein (GFP) variants SSC and W7. W7 fluoresces at a shorter wavelength than GFP. The construct comprises a donor (e.g. S6C) and an acceptor (e.g. W7) fluorescent protein moiety (donors and an acceptor can be green or blue fluorescent proteins), and a linker coupling them. Preferably, the donor is positioned at the N-terminus of the polypeptide relative to the acceptor. The linker moiety is a peptide 5-50 amino acids in length containing a protease cleavage site. In this

```
example, the linker moiety contains many recognition sites for proteases, including trypsin, calpain and enterckinase. The donor and acceptor moieties exhibit fluorescent resonance energy transfer (FRET) when they are cleaved. The constructs are used in enzymatic assays and can be used to isolate new enzyme inhibitors or promoters. The specific activity of enzyme (in vivo and in virto) and compounds altering enzyme activity can be obtained. FRET and hence activity of specific compounds is measured from the acceptor or donor moiety or maybe obtained using a ratio between the two. Note: The present sequence does not appear in the specification; it has been made by modifying the native GFP sequence, and adding the linker moiety in the appropriate place
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                             VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                           NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fluorescent resonance energy transfer; FRET; enzymatic assay; W7; enzyme inhibitor; enzyme promoter; PCR primer; protease cleavage site; Tandem fluorescent protein construct; blue fluorescent protein.
                                                                                                                                                                                                                                                                            1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             North West Pacific jellyfish; green fluorescent protein; GFP; S65C;
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFP variants S65T and W7 tandem fluorescent protein construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= S65C
/note= "wild type Ser substituted with Thr"
239. .264
/label= linker_moeity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Y66W
/note= "wild type Tyr substituted with Trp"
Misc-difference 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188. .259
| label= trypsin_enterokinase_cleavage_site
                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                99.4%; Score 1257; DB 2; 98.7%; Pred. No. 8e-122; ive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250. .251
/label= trypsin_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553. .254
|label= calpain_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .238
/label= S65T_GFP_variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265. .501
/label= W7_GFP_variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW31879 standard; protein; 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.7
Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aequorea victoria.
                                                                                                                                                                                     Sequence 501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW31879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW31879
      8888888888888888
                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

Val substituted with Ala"

```
Tandem fluorescent protein constructs - have donor and acceptor moieties exhibiting fluorescent linked via cleavable peptide linker, useful in
                      Tabel= M153T
note= "wild type Met substituted with Thr"
                                                                          "wild type Asn substituted with Lys"
         'note= "wild type Asn substituted with Leu'
                                            /label= V163A
/note= "wild type
                                                                                                                                                (REGC ) UNIV CALIFORNIA. (AURO-) AURORA BIOSCIENCES CORP.
                                                                  /label= N212K
  label= N146L
                                                                                                                      97WO-US001457.
                                                                                                                                                                          Cubitt A;
                                                                                                                                                                                                                                  Claim 3; Page; 88pp; English.
                                                                                                                                     96US-00594575
                                                                           /note=
                                                                                                                                                                                       WPI; 1997-402615/37
                                                                                                                                                                          Heim R,
                                                                                                                                                                                                                     enzymatic assays.
               Misc-difference
                                     Misc-difference
                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 501 AA;
                                                                                                                      31-JAN-1997;
                                                                                                                                    31-JAN-1996;
                                                                                        WOS728261-A1
                                                                                                       07-AUG-1997
                                                                                                                                                                        Tsien RY,
```

This protein sequence is that of a novel tandem fluorescent protein construct, made using Aequorea victoria (North West Pacific jellyfish) organe fluorescent protein (GFP) variants S657 and W7. W7 fluoresces at a shorter wavelength than GFP. The construct comprises a donor (e.g. 865T) and an acceptor (e.g. W7) fluorescent protein moiety (donors and a ceptors can be green or blue fluorescent protein), and a linker coupling them. Preferably, the donor is positioned at the N-terminus of the polypeptide relative to the acceptor. The linker moiety is a peptide cample, the linker moiety containing a protease cleavage site. In this example, the linker moiety contains many recognition sites for proteases, including trypsin, calpain and enterokinase. The donor and acceptor moieties exhibit fluorescent resonance energy transfer (RRET) when they are cleaved. The constructs are used in enzymatic assays and can be used to isolate new enzymes or enzyme inhibitors or promoters. The specific compounds is measured from the acceptor or donor moiety of specific compounds is measured from the acceptor or donor moiety or maybe obtained using a ratio between the two. Note: The present sequence does not appear in the specification; it has been made by modifying the native GPP sequence, and

```
ö
                                                                                                                             VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                              121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                       443
                                                                                                      323
                                                                                                                                                       9
                                                                                                                                                                                                                                                             181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                        264 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLDVPWPTL
                                                                                                                                                                                                                             NRIBLKGIDFKEDGNILGHKLEYNYLSHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD
                                                                MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                     Gaps
                                       ö
 99.4%; Score 1257; DB 2; Length 501; 98.7%; Pred. No. 8e-122; Live 2; Mismatches 1; Indels
                                  Conservative
               Similarity
Query Match
Best Local Simi
Matches 235;
                                                                                                                               61
                                                                                                                                                                                                                              384
                                                                                           g
                                                                                                                            à
                                                                                                                                                         g
                                                                                                                                                                                           ò
                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                             à
```

compitaing a donor or acceptor fluorescent protein moiety (e.g. jellyfish green fluorescent protein, GFP) or a linker moiety that couples the donor and acceptor moietuse. Also include are a recombinant mucleic acid coding for expression of the tandem fluorescent protein construct, an expression vector comprising expression control sequences operatively linked to a sequence coding for the expression of the tandem fluorescent protein construct, a host cell transfected with the expression vector determining whether a sample contains an enzyme or whether a compound alters the activity of an enzyme, determining the amount of activity of an enzyme, is useful in enzymeactivity. The tandem fluorescent protein construct is useful in enzymeactivity. The tandem fluorescent resonance energy transfer (FRET) between the

The invention relates to a tandem fluorescent protein construct

Claim 18; Page; 34pp; English

```
New tandem fluorescent protein construct comprising a donor or acceptor fluorescent protein moiety or a linker moiety that couples the donor and acceptor moieties, useful in enzymatic assays.
444 HYQQYTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHNVLLEPVTAAGITHGMDELYK 501
                                                                                                                                                       Jellyfish; enzyme; green fluorescent protein; GFP; FRET; mutant;
fluorescent resonance energy transfer; tandem fluorescent protein;
enzymatic assay; Alzheimer's disease; hypertension; inflammation;
apoptosis; AIDS; acquired immunodeficiency syndrome; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                Lya"
                                                                                                                                                                                                                                                                                                            Trp.
                                                                                                                                                                                                                                                                                                                                Ile"
                                                                                                                                                                                                                                                              'note= "Wild-type Phe substituted by
                                                                                                                                                                                                                                                                                    'note= "Wild-type Ser substituted by
                                                                                                                                                                                                                                                                                                                             note= "Wild-type Asn substituted by
                                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Met substituted by
                                                                                                                                                                                                                                                                                                                                                                           substituted by
                                                                                                                                                                                                                                                                                                                                                                                             /note= "Wild-type Asn substituted by
                                                                                                                                                                                                                                                                                                        'note= "Wild-type Tyr
                                                                                                                                                                                                                                                                                                                                                                          note= "Wild-type Val
                                                                                                                                                      Jellyfish; enzyme; green fluorescent
                                                                                                                                                                                                                                            Location/Qualifiers
                                                                 ABG76009 standard; protein; 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heim R, Cubitt A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-00594575,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-2002; 2002US-00057505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00792553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00396003
                                                                                                          (first entry)
                                                                                                                                 Jellyfish GFP mutant W1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-247255/24.
                                                                                                                                                                                                                                                                                                                                       Misc-difference 153
                                                                                                                                                                                                                                                                        Misc-difference 65
                                                                                                                                                                                                          Aequorea victoria.
Synthetic.
                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                   US2002164674-Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-1997;
13-SEP-1999;
                                                                                                           30-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                       07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsien RY,
                                                                                     ABG76009;
                                           RESULT 5
                                                                           g
```

```
donor and acceptor moieties. The tandem fluorescent proteins are particularly useful in assays for protease activity. Proteases play an essential role in many disease processes e.g. Alzheimer's disease, hypertension, inflammation, apoptosis and AIDS (acquired immunodeficiency syndrome). Tandem fluorescent proteins were constructed comprising mutants of GFP with altered fluorescent spectra. The present sequence represents a mutant GFP suitable for incorporation into a tandem fluorescent protein of the invention. Note: The present sequence shown in the specification but was created by the indexer using the information in the specification and the wild-type GFP protein appearing
                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                 61 VITLIWGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                              NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                     HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                     Phenotype selection; non-selectable; fusion protein; stable expression; selectable marker; antibiotic resistance gene; Bscherichia coli; green fluorescent protein; GFP; GFPRI; pGFP; mutant; mutein.
                                                                                                                                                                                                                                                                    1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                          VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                              ;
                                                                                                                                                                                                  Length 238;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Ala replaces wild-type Val"
                                                                                                                                                                                                                              5
                                                                                                                                                                                               Score 1250; DB 6;
Pred. No. 1.4e-121;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Green fluorescent protein mutant, GFPR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB73554 standard; protein; 238
                                                                                                                                                                                                                          .;
7
                                                                                                                                                                                              98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-2000; 2000US-00510097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-2000; 2000WO-US008477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0160461P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry
                                                                                                                                                                                                                        Matches 234; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PANO-) PANORAMA RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-282162/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 163
                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aequorea victoria
                                                                                                                                                                  Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAH20247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200129225-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salint RF;
                                                                                                                                                                                                                                                                                                          19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB73554;
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
 88888888888888888
                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gg
                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

Obtaining cells expressing mutant protein, comprises selecting from cells

```
The invention relates to methods whereby variants of proteins which do not confer selectable phenotypes can be selected for stable expression in confer selectable phenotypes can be selected for stable expression in confer selectable phenotypes can be selected for expression in the host cells, for obtaining a mutant protein with enhanced stability relative to the wild-type protein, and for identifying peptides that stabilise an unstable protein. The methods all involve expressing the protein of interest as a fusion with a protein that can confer a selectable confers as a fusion with a protein that can confer a selectable confers as a fusion with a protein that can confer a selectable contable contable grown under selective pressure (e.g., presence of antibiotic). The cells able to grow under such conditions are those which contain fusion proteins which are optimised for expression or which are contain fusion proteins which are optimised for expression or which are contain fusion proteins which are optimised for expression or which are contain fusion proteins which are optimised for expression or which are contained amount or rate of synthesis of the selectable marker. The invention also discloses mutants of green fluorescent protein (GFPP) selected for sequence represents a GFP mutant (GFPR) which has increased stability calative to wild-type GFP. The present sequence is not shown in the specification, but was derived from the plasmid pGFP (GenBank accession number U17997) and the information given on page 23 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQBRTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VITESYGVQCFSRXPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
transformed with library of mutagenized protein coding sequences joined to selector protein, which confers growth under selective conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; GFP; jellyfish; marker protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Location/Qualifiers
Misc-difference 163
/note= "Ala replaces wild-type Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1242; DB 4;
Pred. No. 9.8e-121;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green fluorescent protein mutant, V163A-GFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reporter protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA25213 standard; protein; 238
                                                            Example 2; Page; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.2%;
97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 97.9
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
Aeguorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Green fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB2374868-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA25213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA25213
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

28-SEP-2001; 2001GB-00023288

Thomas N;

Green fluorescent protein mutant Y66H/Y145F.

```
(GFP) mutuants containing an amino acid substitution at positions 64 and 175, and additionally an amino acid substitution at either proistion 65 or 222. The mutents of the invention are particularly F641-S1750-E222G-GFP (ADA25195) or F641-S677-S175G-GFP (ADA25196). GFP mutants of the invention exhibit enhanced fluorescence relative to wild type GFP when care expressed in non-homologous cells at temperatures above 30 degrees capsus, and excited at 490 nm. The mutants can also be detected in mammalian cells at lower levels of expression and with increased sensitivity relative to wild type GFP. The GFP mutants of the invention are useful as non-toxic markers for selection of transfected cells, as protein labels in living and fixed cells, as markers in cell or organelle fusion, for visualising translocation of intracellular proteins to a specific organelle, as secretion markers, as genetic reporters or protein caps for protein and gene expression in transgenic animals, as cell or organelle integrity markers, as transfection markers, as markers to be used in combination with fluorescent activated cell sorting (FACS), as real-time probes working at near physiological concentrations, for harders and represent activated cell sorting fracting fractions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               performing transposon vector mutagenesis, and as reporters for bacterial detection. The present sequence represents an Aequorea victoria GFP mutant used in an example of the invention. Note: The present sequence is not shown in the specification, but is derived from the wild-type GFP sequence shown in Fig 2 and the information given on page 24.
                                                                                                                                                                                                                                                                                                             Novel fluorescent protein derived from green fluorescent protein useful as a transfection marker, has different excitation spectrum and/or emission spectrum compared with wild-type green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to Aequorea victoria green fluorescent protein
                                                                                                     (AMSH ) AMBRSHAM PHARMACIA BIOTECH UK LTD.
(AMSH ) AMBRSHAM BIOSCIENCES UK LTD.
                                                                                                                                                                                     Michael NP,
                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page; 52pp; English.
                                                    23-APR-2001; 2001GB-00009858.
                                                                                                                                                                               Stubbs SLJ, Jones AE,
                                                                                                                                                                                                                                      2003-095652/09.
                                                                                                                                                                                                                                                            N-PSDB; ADA25193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 238 AA;
```

```
61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                        61 VITESYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                              121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                 9
                                                                                    1 MSKGBELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLFVFWFTL 60
                                                                                                                                                                                                                                                        HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                           1 MSKGEBLFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                    ;
0
   Score 1242; DB 6; Length 238; Pred. No. 9.8e-121; 1; Mismatches 4; Indels
                                  Indels
   98.2%;
                                Conservative
Query Match
Best Local Similarity
                             Matches 233;
                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                            g
                                                                                      g
                                                                                                                    à
                                                                                                                                          S
C
                                                                                                                                                                           à
                                                                                                                                                                                                       В
                                                                                                                                                                                                                                     à
```

AAW05310 standard; protein; 238 AA

(first entry)

02-APR-1997

AAW05310;

AAW05310 1D AAW0 XX AC AAW0 XX DT 02-A

RESULT 8

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW05305-W05312 represent Aequorea victoria (jellyfish) green fluorescent protein (GFP) of the invention (see AAW05304 for the wild type protein). The fluorescence of this protein is generated by cyclisation and coxidation of the Ser-This protein is generated by cyclisation and the related GFP from the sea paisty (Renilla reniformis). The modifications present in these sequences were created by subjecting the CDNA encoding this sequence to site directed mutagenesis using mutagenic CPK primers, or hydroxylamine treatment. These GFPs of the invention are modified to lead to the formation of products with markedly different excitation and emission spectra. Visibly distinct colours, and increased contacts a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTIFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VITFSHGVQCFSRYPDH#KRHDFFKSAMPEGYVQBRTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contexts, such as tracking of differential gene expression and protein localisation. The mutations can also be created to modify the encoded GPP so that it only possesses one absorbance peak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NRIELKGIDFKEDGNILGHKLEYNFNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVOLAD 180
                                                  Green fluorescent protein, GPP, jellyfish, Aequorea victoria, sea pansy, Renilla reniformis, differential gene expression, protein localisation, gene expression tracking, fluorescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New modified Aequorea green fluorescent polypeptide(s) - having amino acid changes to provide prods. which exhibit different excitation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRIELKGIDFKEDGNILGHKLEYNFISHNYYITADKQKNGIKANFKIRHNIEDGSVQLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1241; DB 2;
Pred. No. 1.2e-120;
0; Mismatches 5;
                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page ?; 39pp; English.
                                                                                                                                                                                                                                                                                                                                          /note= "Y145F"
                                                                                                                                                                                                                                                                                  /note= "Y66H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95WO-US014692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-00337915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-371370/37
                                                                                                                                                                                                                                                                                                             Misc-difference 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                  Misc-difference 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rsien RY, Heim R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  emission spectra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                WO9623810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-1996
                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

us-10-057-505-2-copy.rag

7

```
Jellyfish; enzyme; green fluorescent protein; GFP; FRET; mutant; fluorescent resonance energy transfer; tandem fluorescent protein; enzymatic assay; Alzheimer's disease; hypertension; inflammation; apoptosis; AlDS; acquired immunodeficiency syndrome; mutein.
                                                                                                                                           /note= "Wild-type Tyr substituted by His"
                                                                                                                                                         /note= "Wild-type Tyr substituted by Phe"
                                                                                                                            Location/Qualifiers
       ABG76005 standard; protein; 238 AA.
                                                                                                                                                                                                                   96US-00594575.
97US-00792553.
99US-00396003.
                                                                                                                                                                                                                                                              Tsien RY, Heim R, Cubitt A;
                                                                                                                                                                                                     25-JAN-2002; 2002US-00057505.
                                    (first entry)
                                                   Jellyfish GFP mutant P4-3
                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                             WPI; 2003-247255/24.
                                                                                                      Aequorea victoria
                                                                                                                                   Misc-difference
                                                                                                                                                  Misc-difference
                                                                                                                                                                        JS2002164674-A1
                                                                                                                                                                                                                   31-JAN-1996;
31-JAN-1997;
13-SEP-1999;
                                    30-APR-2003
                                                                                                                                                                                      07-NOV-2002
                                                                                                              Synthetic.
                      ABG76005;
ABG76005
```

The inventor of the control of control of control of the control of the control of the control of control, an expression of the control of the control of the control of the control of control, a host call transfected with the expression vector, of control, a host call transfected with the expression vector, of an enzyme of an enzyme, determining the amount of activity of an enzyme in a call and testing for cleavage enzyme activity. The tandem fluorescent protein construct is useful in enzymatic assays, using the control of the control of activity of an enzyme in a call and testing for cleavage enzyme activity. The tandem fluorescent proteins are controlarly useful in assays for protease activity. Proteases play an experiental role in many disease processes e.g. Alzheimer's disease, bypertension, inflammation, apoptosis and AIDS (acquired immondeficiency syndrome). Tandem fluorescent proteins were constructed comprising contains of GFP with altered fluorescent spectra. The present sequence fluorescents protein of the invention. Note: The present sequence conformation in the specification but was created by the indexer using the information in the specification and the wild-type GFP protein appearing as an ansample of information in the specification and the wild-type GFP protein appearing New tandem fluorescent protein construct comprising a donor or acceptor fluorescent protein moiety or a linker moiety that couples the donor and acceptor moieties, useful in enzymatic assays. The invention relates to a tandem fluorescent protein construct Claim 3; Page; 34pp; English.

Sequence 238 AA;

```
ö
                                                                                                                                                        61 VITESHGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIFFKDDGNYKTRAEVKFEGGDILV 120
                                                                                                                                         120
                                                                                                        60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to chimeric phosphorylation indicators comprising a phosphorylation polypeptide and a fluorescent protein or in operative linkage, a donor molecule, a phosphorylatable domain, a phosphoaminoacid binding domain (PAABD) and an acceptor molecule. The phosphoaminoacid binding domain (PAABD) and an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting kinases or phosphatases in a biological sample. They are also useful in high throughput analysis e.g. for detecting a kinase inhibitor or phosphatase inhibitor. The present sequence is Aequorea victoria mutant green fluorescent protein (GFP; NH461) used in the invention. Note: This sequence is not shown in the specification but is derived from Aequorea victoria wild-type GFP shown as SEQ ID NO: 2 in column 53-54 of the
                                                                                                                                                                                                                                                                         181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                              Phosphorylation indicator, fluorescent protein, detection, phosphatase, kinase, green fluorescent protein, GFP, mutant, mutein.
                                                                                                                                                                                                                           1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                    VITFSXGVQCFSRYPDHMXRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
                                                                                                                                                                                                      NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel chimeric phosphorylation indicators, useful for detecting kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in operative linkage.
                                      ·:
       Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Asn substituted with Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aequorea victoria mutant green fluorescent protein (N146I).
                                                                   1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICT
                                      Indels
   Score 1241; DB 6;
Pred. No. 1.2e-120;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          AAE34991 standard; protein; 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Col; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang J;
 98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-2001; 2001US-00865291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-2002; 2002WO-US016955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ting AY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-148474/14
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200295058-A2
Query Match
Best Local Simil
Matches 233; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isien RY,
                                                                                                                                      61
                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                             AAE34991;
                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                            AAE3499.
                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                  d
                                                                                                                                                                                                    à
                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                                   g
```

```
AAW31876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW31876
ID AAW
XX
   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                     ö
                                                                                                   VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                              61 VTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                               121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                     9
                                                                                     9
                                                                                                                                                                       HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                 North West Pacific jellyfish, green fluorescent protein, GFP, P4-3, fluorescent resonance energy transfer; FRET; enzymatic assay; W7; enzyme inhibitor; enzyme promoter; PCR primer; protease cleavage site; Tandem fluorescent protein construct; blue fluorescent protein.
                                                                               1 MSKGEELFIGUVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                   1 MSKGEBLFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                     Gaps
                                                   .;
0
                                                                                                                                                                                                                                                                                    GFP variants P4-3 and W7 tandem fluorescent protein construct.
                                    Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "wild type Met substituted with Thr"
                                                                                                                                                                                                                                                                                                                                                                                                          /label= Y66H
/note= "wild type Tyr substituted with His"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "wild type Tyr substituted with Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "wild type Asn substituted with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .259
| Jabel = trypsin_enterokinase_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "wild type Tyr substituted with Trp'
                                                   4; Indels
                                  Score 1241; DB 6;
Pred. No. 1.2e-120;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 .251
/label= trypsin_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253. .254
/label= calpain_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                         /label= P4-3_GFP_variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65. .501 - Tabel= W7_GFP_variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                    239. .264
/label= linker_moeity
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                 2;
                                                                                                                                                                                                                                 AAW31880 standard; protein; 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 426
/label= V163A
                                                                                                                                                                                                                                                                                                                                                                                                                                    'label= Y145F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= N146L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= M153T
                                 98.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Y66W
                                                                                                                                                                                                                                                                   03-FEB-1998 (first entry)
                                                 Matches 232; Conservative
specification (AAE34957)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 416
                                         Similarity
                                                                                                                                                                                                                                                                                                                                                        Aequorea victoria
                 Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage-site
                                                                                                                                                                                        181
                                                                                                    61
                                Query Match
                                                                                                                                                                                                                                                   AAW31880;
                                          Local
                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                        SXS
                                                                                  엄
                                                                                                                 gg
                                                                                                                                                    셤
                                                                                                                                                                                   qq
                                                                   à
                                                                                                   à
                                                                                                                                  à
                                                                                                                                                                      ö
```

```
This protein sequence is that of a novel tandem fluorescent protein

Construct, made using Aequorea victoria (North West Pacific jellyfish)

green fluorescent protein (GFP) variants P4-3 and WT. Both of these

fluoresce at a shorter wavelength than GFP. The construct comprises a

donor (e.g. P4-3) and an acceptor (e.g. W7) fluorescent protein moiety

(donors and acceptors can be green or blue fluorescent protein moiety

inher coupling them. Preferably, the donor is positioned at the N-

terminus of the polypeptide relative to the acceptor. The linker moiety

is a peptide 5-50 amino acids in length containing a protease cleavage

site. In this example, the linker moiety contains many recognition sites

for proteases, including trypsin, calpain and enterchinase. The donor and

acceptor moieties exhibit fluorescent resonance energy transfer (FRET)

when they are cleaved The constructs are used in enzymatic assays and

can be used to isolate new enzymes or enzyme inhibitors or promoters. The

specific activity can be obtained. FRET and hence activity of specific

conzyme activity can be obtained. FRET and hence activity of specific

conzyme activity can be obtained. FRET and hence activity of specific

conzyme activity of enzyme (in vivo and in vitro) and compounds altering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compounds is measured from the acceptor or donor moiety or maybe obtained using a ratio between the two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VITFSHGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRIBLKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIBDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NRIELKGIDFKEDGNILGHKLEYNFNSHNVYIMADKOKNGIKVNFKIRHNIEDGSVOLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tandem fluorescent protein constructs - have donor and acceptor moieties exhibiting fluorescent linked via cleavable peptide linker, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTIGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 501;
                                                                       /label= N212K
/note= "wild type Asn substituted with Lys"
/note= "wild type Val substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.1%; Score 1241; DB 2; 97.9%; Pred. No. 3.7e-120; iive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW31876 standard; protein; 514 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA.
(AURO-) AURORA BIOSCIENCES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsien RY, Heim R, Cubitt A;
                                                                                                                                                                                                                                                                                                                                                         97WO-US001457
                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-00594575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 97.9°
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-402615/37
                                          Misc-difference 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzymatic assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 501 AA;
                                                                                                                                                                                                                                                                                                                                                             31-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-1996;
                                                                                                                                                                                                                                                                             07-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
```

ö

σ

ö

Gaps

·,

5,

Length 514; Indels 9

Synthetic.

Protein

Peptide

Peptide

```
Cleavage-site
                       Cleavage-site
                                   WO9728261-A1
                                         31-JAN-1996;
                                     07-AUG-1997
                           Protein
```

11-JAN-1997;

(AURO-)

Cleavage-site

```
activity of enzyme (in vivo and in vitro) and compounds altering enzyme activity can be obtained. FRET and hence activity of specific compounds is measured from the acceptor or donor molety or maybe obtained using a ratio between the two. Note: The present sequence does not appear in the specification; it has been made by modifying the native GFP sequence, and adding the linker molety in the appropriate place
                                                                                                                                                                                                                                                                                                                                                                                                           337 VITFSHGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 NRIELKGIDFKEDGNILGHKLEYNFNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYQQNTPIGDGFVLLPDNHYLSTQSALSKDPNEKRDHWYLLEFVTAAGITHGMDELYK 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phenotype selection; non-selectable; fusion protein; stable expression; selectable marker; antibiotic resistance gene; Escherichia coli; green fluorescent protein; GFP; GFPuv; pGFPuv; mutant; mutein.
                                                                                                                                                                                                                                                                                                                              277 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                         VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV
                                                                                                                                                                                                                                                                                     1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                   Score 1241; DB 2;
Pred. No. 3.8e-120;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Green fluorescent protein variant GFPuv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB73553 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-2000; 2000US-00510097.
                                                                                                                                                                                                     98.1%;
97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-2000; 2000WO-US008477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0160461F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                     al Similarity 97.9
233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PANO-) PANORAMA RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-282162/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    victoria
                                                                                                                                                          Sequence 514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH20246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200129225-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                               Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB73553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aequorea
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB73553
    8888888
                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \dot{\delta}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This protein sequence is that of a novel tandem fluorescent protein

Construct, made using Aequorea victoria (North West Pacific Jellyfish)

green fluorescent protein (GFP) variants S65C and P4-3. P4-3 fluoresces

at a shorter wavelength than GFP. The construct comprises a donor (e.g.,

S65C) and an acceptor (e.g. P4-3) fluorescent protein moiety (donors and
acceptors can be green or blue fluorescent proteins), and a linker

acceptors can be green or blue fluorescent proteins and linker

coupling them. Preferably, the donor is positioned at the N-terminus of
the polypeptide relative to the acceptor. The linker moiety is a peptide

5-50 amino acids in length containing a protease cleavage site. In this
example, the linker moiety contains many recognition sites for proteases,
including trypsin, calpain and enterokinase. The donor and acceptor
moieties exhibit fluorescent resonance energy transfer (FRET) when they

are cleaved. The constructs are used in enzymatic assays and can be used
to isolate new enzymes or enzyme inhibitors or promoters. The specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tandem fluorescent protein constructs - have donor and acceptor moieties exhibiting fluorescent linked via cleavable peptide linker, useful in
                                                                                               North West Pacific jellyfish; green fluorescent protein; GFP; S65C; fluorescent resonance energy transfer; FRET; enzymatic assay; P4-3; enzyme inhibitor; enzyme promoter; PCR primer; protease cleavage site; Tandem fluorescent protein construct; blue fluorescent protein.
                                                      GFP variants S65C and P4-3 tandem fluorescent protein construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with His"
                                                                                                                                                                                                                                                                                                                                                                                                       /label= 865C
/note= "wild type Ser substituted with Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270. .271
/label= trypsin_enterokinase_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "wild type Tyr substituted with Phe'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note≈ "wild type Tyr substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1= trypsin_cleavage_site
.266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calpain_cleavage_site
                                                                                                                                                                                                                                                                                                     '. .10
'label= polyhistidine_tag
                                                                                                                                                                                                                                                                                                                                         252. .276
/label= linker_moiety
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AURORA BIOSCIENCES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Y145F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US001457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-00594575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Y66H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cubitt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262. .263
/label= try
           03-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-402615/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'sien RY, Heim R,
                                                                                                                                                                                                                                 Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enzymatic assays.
                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
```

Obtaining cells expressing mutant protein, comprises selecting from cells transformed with library of mutagenized protein coding sequences joined to selector protein, which confers growth under selective conditions.

Example 2; Page; 52pp; English.

The invention relates to methods whereby variants of proteins which do not confer selectable phenotypes can be selected for stable expression in host cells (especially Escherichia coli). The methods can be used to obtain mutants of a desired protein optimised for expression in the host

```
cells, for obtaining a mutant protein with enhanced stability relative to the wild-type protein, and for identifying peptides that stabilise an unstable protein. The methods all involve expressing the protein of interest as a fusion with a protein that can confer a selectable of stabilise an antibiotic resistance protein. The transformed host cells are then grown under selective pressure (e.g., presence of antibiotic). The cells able to grow under such conditions are those which contain proteins which are optimised for expression or which are more stable, as this property will also correlate with an increased amount or rate of synthesis of the selectable marker. The invention also discloses mutants of green fluorescent protein (GFP) selected for increased stability using the method of the invention. The present sequence is not shown in the specification of the invention. The present sequence is not shown in the specification, but was derived for thom GenBank decession number U62636
                                                                                                                                                                                                                                                                                                                                                                                                                                  VTIFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKIRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VITESYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIISFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRIBLKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation indicator; fluorescent protein; detection; phosphatase;
                                                                                                                                                                                                                                                                                                                                                                                         1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                         Score 1240; DB 4; Length 238; Pred. No. 1.6e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aequorea victoria mutant green fluorescent protein (M153T).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild-type Met substituted with Thr"
                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase; green fluorescent protein; GFP; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE34992 standard; protein; 238
                                                                                                                                                                                                                                                                                                       98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-2002; 2002WO-US016955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 97.9°
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aequorea victoria
                                                                                                                                                                                                                                                                         Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200295058-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE34992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

ö

Gaps

. 0

9 9

```
61 VITESYGVQCFSRXPDHMKQHDFFKSAMPEGYVQBRIIFFKDDGNYKTRAEVKFBGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VITESXGVQCFSRYPDHMKRHDFFKSAMPEGYVQBRTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to chimeric phosphorylation indicators comprising a phosphorylation polypeptide and a fluorescent protein or in operative linkage, a donor molecule, a phosphorylatable domain, a phosphoaminoacid binding domain (PAABD) and an acceptor molecule. The phosphoaminoacid binding domain (PAABD) and an acceptor molecule. The phosphorylation indicators of the invention are useful for detecting kinases or phosphatases in a biological sample. They are also useful in high throughput analysis e.g. for detecting a kinase inhibitor or phosphatase inhibitor. The present sequence is Aequorea victoria mutant green fluorescent protein (GFP; MIS3T) used in the invention. Note: This sequence is not shown in the specification but is derived from Aequorea victoria wild-type GFP shown as SEQ ID NO: 2 in column 53-54 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMYLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green fluorescent protein; GFP; jellyfish; Aequorea victoria; sea pansy Renilla reniformis; differential gene expression; protein localisation; gene expression tracking; fluorescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
             Novel chimeric phosphorylation indicators, useful for detecting kinase/phosphatase in samples, has donor molecule, phosphorylatable domain, phosphoaminoacid binding domain, and acceptor molecule, in operative linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFP mutant Y66W/I123V/Y145H/H148R/M153T/V163A/N212K.
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1240; DB 6;
Pred. No. 1.6e-120;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW05311 standard; protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "M153T"
163
/note= "V163A"
                                                                                                         Disclosure; Col; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Y66W"
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 97.5%;
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                    specification (AAE34957)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW05311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW05311
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsien RY, Ting AY, Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAY-2001; 2001US-00865291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-148474/14
```

```
AAW05305-W05312 represent Aequorea victoria (jellyfish) green fluorescent protein (GFP) of the invention (see AAW05304 for the wild type protein.

The fluorescence of this protein is generated by cyclisation and oxidation of the Ser-Tyr-Gly sequence at positions 65-67. Aequore GFP has two absorbance peaks, as opposed to the one absorbance peak seen in the related GFP from the sea pansy (Renilla rentiformis). The modifications present in these sequences were created by subjecting the cDNA encoding this sequence to site directed mutagenesis using mutagenic PCR primers, or hydroxylamine treatment. These GFPs of the invention are modified to lead to the formation of products with markedly different excitation and emission spectra. Visibly distinct colours, and increased intensities of emission make these products useful in a wide variety of contexts, such as tracking of differential gene expression and protein localisation. The mutations can also be created to modify the encoded GFP so that it only possesses one absorbance peak
                                                                                                                                                                                                                                                                                                                                                       New modified Aequorea green fluorescent polypeptide(s) - having amino acid changes to provide prods. which exhibit different excitation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.9%; Score 1239; DB 2; Length 238; Best Local Similarity 97.9%; Pred. No. 2e-120; Matches 233; Conservative 1; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page ?; 39pp; English.
Misc-difference 212
/note= "N212K"
                                                                                                                                                  95WO-US014692
                                                                                                                                                                                         94US-00337915
                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                WPI; 1996-371370/37
                                                                                                                                                                                                                                                                       Isien RY, Heim R;
                                                                                                                                                                                                                                                                                                                                                                                                  emission spectra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 238 AA;
                                                                                                                                                13-NOV-1995;
                                                                                                                                                                                         10-NOV-1994;
                                                                WO9623810-A1
                                                                                                         08-AUG-1996.
```

1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 0; Gaps ò

ö

9

61 VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120 61 VITTESWGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180 121 g à Db à

à

Search completed: April 19, 2004, 15:05:58 Job time : 61 secs

13.

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

April 19, 2004, 14:56:35 ; Search time 17 Seconds (without alignments) 728.982 Million cell updates/sec

US-10-057-505-2-COPY
1265
1 MSKGEELFTGVVPILVELDG......VLLEFVTAAGITHGMDELYK 238 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	rea	pp92 campyloba			_											P17655 homo sapien		P24506 discopyqe o		Q48449 klebsiella					Q87c65 xylella fas							_	
SUMMARIES	ΠD	GFP AEQVI	TRMA CAMJE	PEPF MYCPU	DPOE YEAST	AC2L_HUMAN	AMPA WIGBR	ITH3 MESAU	SYL_XYLFA	D152_HAEIN	D151 HAEIN	SET7_HUMAN	ACS2_RHIME	STRH STRPN	CP51 CANGA	NIFD_CLOPA	CAN2 HUMAN	CAN2 MACFA	SY62 DISOM	K6PF METJA	YC03 KLEPN	D153_HAEIN	SLAP_BACLI	SPED_CLOAB	CAN2 RABIT	SYL_XYLFT	TRMB HELPJ	AC2L_MOUSE	BAG STRAG	HKRI YEAST	TP6B_SULSH	ITH3 RAT	LONH PYRHO	COPA_HUMAN
	DB	н	П						Н																			Н	Н	Н	н	н	-1	Н
	Length	238	357	613	2222	689	501	886	879	795	797	366	649	1312	533	533	700	700	439	462	504	793	874	274	422	879	400	68	1164	1802	530	887	1127	1224
* Query	Match	•		٠	•	6.7			6.5	•	•		•	6.4	•	6.4	6.4	٠	•	6.3	٠	•	٠	•	•	•	•	•	٠	•	•	6.2	•	•
	Score	1234	87.5	87.5	85.5	82	84.5	84.5	82.5	82	82	81	81		0	80.5	0	0	80	80	80	80	80	79.5	79.5	79.5	79	79	79	79	78.5	78.5	78.5	78.5
Result	No.	Н	Ŋ	m	4	Ŋ	φ	7	œ ·	σ.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	26	27	28	29	30	31	32	e E

027971 bos taurus	P57203 buchnera ap	P23212 staphylococ	Ogpaco ureaplasma	P43367 sus scrofa	P07354 gallus gall	Q8dvs2 streptococc	Q27954 bos taurus	P58555 anabaena sp	09kwa3 agrobacteri	P58132 astasia lon	Q14721 homo sapien
CAN2 BOVIN	HIS' BUCAI	MSRA STAEP	SYL_UREPA	CANZ PIG	PLK CHICK	PEPX_STRMU	COPA_BOVIN	RCA ANASP	ACSA AGRRH	RPOD_ASTLO	KCB1_HUMAN
	4	-	-	н	-	Н	-	-	Н	Н	4
207	353	488	806	324	355	758	1224	414	652	817	828
6.2	7.0	6.2	6.2	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1
78	80	78	78	77.5	77.5	77.5	77.5	77	77	77	77
6. c	9	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

```
SEQUENCE FROM N.A.

MEDLINE=97299832; PubMed=9154981;
Rouwendal G.J.A., Mendes O., Wolbert E.J.H., de Boer A.D.;
Finhanced expression in tobacco of the gene encoding green fluorescent protein by medification of its codon usage.";
Plant Mol. Biol. 33:989-999(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93192221; PubMed=8448132; Cody C.W., Prasher D.C., Ward W.W.; "Chemical structure of the hexapeptide chromophore of the Aequorea
                                                                                                                              Aequorea victoria (Jellyfish).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
WCBI_TaxID=6100;
                                                                                                                                                                                                                                                                                                                                                                                                                gene and
                                                                                                                                                                                                                                                                                              "Primary structure of the Aequorea victoria green-fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trystal structure of the Aequorea victoria green fluorescent
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=94185810; PubMed=8137953;
Inouye S., Tsuji F.I.;
"Aequorea green fluorescent protein. Expression of the gene fluorescence characteristics of the recombinant protein.";
EERS_Lett__341:277-280(1994).
                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=92175527; PubMed=1347277;
Prasher D.C., Eckenrode V.K., Ward W.W., Prendergast F.G.,
Cormier M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=98294543; PubMed=9631087;
Yang F., Moss L.G., Phillips G.N. Jr.;
"The molecular structure of green fluorescent protein.";
Nat. Biotechnol. 14:1246-1251(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X.RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=96355665; PubMed=8703075;
<u>Ormoe M., Cubitt A.B., Kallio K., Gross L.A., Tsien R.Y.</u>
                              GFP_AEQVI STANDARD; PRT; 238 AA. P42212; 017104; 027903; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          green-fluorescent protein.";
Biochemistry 32:1212-1218(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cience 273:1392-1395(1996)
                                                                                                                                                                                                                                                                                                                              Gene 111:229-233(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHROMOPHORE
                                                                                                                                                                                                                                                                                                                 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
RESULT 1
GFP_AEQVI
```

```
61 VITESYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                            5-imidazolinone (Ser-Gly).
2,3-DIDEHYDROTYROSINE.
F -> Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26886 MW; EASAGF21FBFB6E05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1234; DB 1; L
Pred. No. 2.3e-95;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                             'JDB; ZEMN; 20-AUG-97.
PDB; ZEMN; 20-AUG-97.
EDB; ZEMO; 20-AUG-97.
InterPro; IPR009017; GFP_like.
ThterPro; IPR000786; Green_fl_protein.
                                                                                                             Pfan, PF01353; GFP, 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green_fl_protein; 1.
                                                                                                                                                                                                       97.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                           28
27
27
27
27
27
27
27
27
27
27
27
27
27
                                                                                                                                                                                      66
100
108
1141
219
25
25
80
80
                          28-OCT-98.
20-AUG-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217
238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                         Luminescence;
CROSSLNK
                          1YFP;
2EMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local &
                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                      MOD RES
VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                   STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TURN
STRAND
TURN
STRAND
TURN
STRAND
TURN
STRAND
TURN
STRAND
STRAND
TURN
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TURN
HELIX
STRAND
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAND
                                                                                                                                                                                                                                                                                                                                                         STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                              HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HELIX
                                                                                                                                                                                                                                                                                                                                                                       TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                  TURN
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dp
                                                                                                                                                                                                                                                                                                                  1- TISSUE SPECIFICITY: Photocytes.

1- TISSUE SPECIFICITY: Photocytes.

1- PIM: Contains a covalently attached chromophore, which is composed of modified animo acid residues. The chromophore is formed upon cyclization of the residues Ser-dehydroTyr-Gly.

1- BIOTECHNOLOGY: Has become a useful and ubiquitous tool for making chimeric proteins of GFP linked to other proteins where it functions as a fluorescent protein ed GFP tolerates N-and C-terminal fusion to a broad variety of proteins. It has been expressed in bacteria, yeast, slime mold, plants, Drosophila, zebrafish, and in mammalian cells. As a noninvasive fluorescent marker in living cells, it allows for a wide range of applications where it may function as a cell lineage tracer, reporter of gene expression, or as a measure of protein-protein interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch)
         X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMMISSION
                                                                                                                        MEDLINE-99228303 bubMed-1020315.

Elsiger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;

Elsiger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;

"Structural and spectral response of green fluorescent protein

"structural and spectral response of green fluorescent protein

Biochemistry 38:5296-5301(1999).

-!- FUNCTION: Energy-transfer acceptor. Its role is to transduce the

blue chemiluminescence of the protein aequorin into green

fluorescent light by energy transfer. Fluoresces in vivo upon

receiving energy from the Ca(2+)-activated photoprotein aequorin.

Absorbs light maximally at 395 nm and exhibits a smaller

absorbance peak at 470 nm. The fluorescence emission spectrum

peaks at 509 nm with a shoulder at 540 nm.
                       MEDLINE-98455509; PubMed-9782051; Wachter R.M., Blsliger M.A., Kallio K., Hanson G.T., Remington S.J.; "Structural basis of spectral shifts in the yellow-emission variants of green fluorescent protein."; Structure 6:1267-1277(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE=Issue 11 of June 2001;
WWW="http://www.expasy.org/spotlight/articles/sptlt011.html".
                                                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M62654; AAA27722.1; -. EMBL; M62653; AAA27721.1; -. EMBL; L29345; AAA58246.1; -. EMBL; X96418; CAA65278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1EMA; 08-NOV-96.
1EMB; 16-JUN-97.
1EMC; 20-AUG-97.
1EMG; 20-AUG-97.
1EMG; 12-MAY-99.
1EMK; 20-AUG-97.
1EMK; 20-AUG-97.
1EMK; 20-AUG-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JAN-03.
28-AUG-02.
10-APR-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1B9C; 17-NOV-00.
1BFP; 07-JUL-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1C4F; 14-JUN-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS0692; JQ1514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGFL;
IHCJ;
IHUY;
IJBY;
```

+++

ô

Gaps ö

Length 238; Indels 9 9

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 --LKGIDFKEDGNILGHKLEYNFISHNVYI-TADKQKNGIKANFKIRH-----NIEDGSV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 QLADHYQQNTPIGDGPVLLPDNHYLSTQSALS-----KDPKEKRDHMVLLEFVTAAG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 SXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIE
                                                                                                                                                                                                                                                                                 "The complete genome sequence of the murine respiratory pathogen
                                                                                                                              Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL445503;
PIR; A99552, A99552.
Mypulist; MYPU 3210;
InterPro; IRR006625; Pept M Zn BS.
InterPro; IRR001567; Peptidase M3.
InterPro; IRR011567; Peptidase M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Complete proteome.
395 ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY)
ZINC (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                             MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galie
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.9%; Score 87.5; DB 1; Length 613; Best Local Similarity 22.6%; Pred. No. 8.3; Matches 43; Conservative 38; Mismatches 74; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3504AA247096FAF1 CRC64;
                                                                                                                                                                                                                                                                                                           MOLGIC ACIGE Res. 29:2145-2153 (2001).
-1- COFACTOR: Binds 1 zinc ion (By similarity)
-1- SIMILARITY: Belongs to peptidase family M3
                                    16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Oligoendopeptidase F homolog (EC 3.4.24.-).
     613 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2222 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL445564; CAC13494.1; -.
                                  (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72339 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 ITHGMDELYK 238
                                                                                                                                                                                                                                                                                                Mycoplasma pulmonis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: | ||||
163 VSRGNIELYK 172
                                                                                                    PEPF OR MYPU 3210.
Mycoplasma pulmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     613 AA;
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=2107;
                                                                                                                                                                                                   STRAIN=UAB CTIP
                                                                                                                                                                                                                                                               Blanchard A.;
                               16-OCT-2001
16-OCT-2001
PEPF MYCPU
Q98QPO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPOE YEAST
ID DPOE YEAST
AC P21951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

7;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 34 kDa, 30 kDa, AND 29 kDa)
-1- SUBUNIT: CONSISTS LOCATION: Nuclear.
-1- SUBCELLUIAN LOCATION: Nuclear.
-1- DOWAIN: THE DNA POLYMERASE ACTIVITY DOMAIN RESIDES IN THE N-TERMINAL HALF OF THE PROTEIN, WHILE THE C-TERMINUS IS NECESSARY FOR COMPLEXING SUBUNITS B AND C.
-1- MISCELLANEOUS: In eukaryotes there are five DNA polymerases: alpha, beta, gamma, delta, and epsilon which are responsible for different reactions of DNA synthesis.
-1- SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                                                                                                                                           STRAIN=S288c / FY1679;
MEDLINE=96310631; PubMed=8740425;
Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.;
The sequence of a 24,152 bp segment from the left arm of chromosome XIV from Saccharomyces cerevisiae between the BNI1 and the POL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "DNA polymerase II, the probable homolog of mammalian DNA polymerase epsilon, replicates chromosomal DNA in the yeast Saccharomyces
                                                                                                                           Eukaryota; Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 11:733-740(1992).
-!- FUNCTION: DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA
REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEMPERATURE SENSITIVE MUTANTS.
MEDLINE=92164663; PubMed=1537345;
Araki H., Ropp P.A., Johnson A.L., Johnston L.H., Morrison A.,
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA polymerase epsilon, catalytic subunit A (EC 2.7.7.7) (DNA polymerase II subunit A).
POLZ OR DUNZ OR YNLZ62W OR N0825.
                                                                                                                                                                              Pfam; PF00136; DNA pol B; 1. —
Pfam; PF00136; DNA pol B; 1. —
SMART; SM00486; POLBC; 1. —
SMART; SM00486; POLBC; 1. —
PROSITE; PS00116; DNA POLYMERASE B; FALSE NEG.
Transferase; DNA-directed DNA polymerase; DNA replication;
DNA-binding; Zinc-finger; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGD: S0005206; POLZ.
GO; GO:0000731; P:DNA repair synthesis; IMP.
InterPro; IPR066172; DNA_pol_B.
InterPro; IPR066134; DNA_pol_B dom.
InterPro; IPR066133; DNA_pol_B_exo.
                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M60416; AAA88711.1; -.
EMBL; X92494; CAA63235.1; -.
EMBL; Z71538; CAA96169.1; -.
                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-2221 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A36028; A36028.
GermOnline; 143268; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (east 12:505-514(1996)
                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugino A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---
```

```
REDINE-21638749; PubMed=11780052;

REDINE-21638749; Related R.N., Beard L.M., Beare D.M.,

REDINES S., Cabley V.B., Calmer R.B., Bridgeman A.M., Brown A.J.,

REDINES S., Cobley V.B., Collier R.E., Cannor R.E., Corby N.R.,

Coulson A., Coville G.J., Deadman R.D., Dunn M.R.,

REDINGTON A.G., Frankland J.A., Fraser A., French L., Garner P.,

REDINGTON A.G., Frankland J.A., Roadman R.B., Honden P.J.,

REDINGTON A.G., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RAMEN D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Lawlor S.,

RAMEN D.V., Martin S.E., Jekosech K., Johnson D.,

RAMEN D.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RAMEN D.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RAMEN D.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RAMINE S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RAMINE B.J.C.T., Prathalingam S.R., Plumb R.W., Ramesay H.,

RAMINE B.J.C.T., Prathalingam S.R., Plumb R.W., Ramesay H.,

RAMINE B.J., Cott C.E., Schrad C.A., Sulston J.E.,

RAMINE B.J., Tromans A.C., Vaudin M., Wallis J.M.,

RAMITCHEACY A., Tromans A.C., Vaudin M., Wallis J.M.,

Mitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

Minner R., Wang P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RAMING R. Was R. W., Hubbard T., Durbin R.M., Bentley D.R., Rames R.,

RAMING R. Was R. W., Rubbard T., Durbin R.M., Bentley D.R., Rames R.,

RAMING R. Was R. W., Rubbard T., Durbin R.M., Bentley B.K., Beck S.,

RAMING R. Was R. W., Rubbard T., Durbin R.M., Bentley B.K., Beck S.,

RAMING R. Was R. W., Rubbard T., Durbin R.M., Bentley S.,
                                                                                                                                                                                                                                                            942
                                                                                                                                                                                                                                                                                                 99 FFKDDGNYKTR--AEVKFEGDTLVNR-----IELKGIDFKEDGNILGHKLEYNFI 146
                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                883 LPKSFPETYFFTLENGKKLYLSPPCSMLNYRVHQKFTNHQYQELKDPLNYIYETHSENTI
                                                                                                                                                                                                          53 LPVPWP-TLVTTFSXGVQCFSRYPDHM------KRHDFFKSAMPEGYV----QERTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUB-Brain, and Testis;
MEDLINE=22386257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                   31;
                                                                                                                   DB 1; Length 2222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC2L HUMAN STANDARD; PRT; 689 AA.
Q9NUB1; Q81V99; Q8N234; Q96J11; Q96JX6; Q9NU28;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoration update)
ACCT-2003 (Rel. 42, Last amoration update)
ACCT-2003 (Rel. 42, Last amoration update)
ACCT-2013 (Rel. 42, Last amoration update)
ACCT-2013 (Rel. 42, Last amoration update)
ACCT-2013 (Rel. 42, Last amoration update)
  B1 POTENTIAL.

44 M -> I (IN POL2-9 TS MUTANT).

P -> S (IN POL2-18 TS MUTANT).

255669 MW, CHCDDE2AB147D65B CRC64;
                                                                                                                                                                 50; Indels
                                                                                                                                                                 13; Mismatches
                                                                                                                                           Pred. No. 56;
                                                                                                                   6.8%; Score 85.5;
                                                                                                                                      28.2%;
                                                                                                                                  Local Similarior
hes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       1000 SDIFKVFLEGD 1010
                                                                                                                                                                                                                                                                                                                                                                                          147 S--HNVYITAD 155
  2181
644
710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 414:865-871(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence and
                                                                   2222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAS2L OR XIAA1846
  2108
644
710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rogers J.;
ZN FING
VARIANT
VARIANT
                                                                     SEQUENCE
                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The DNA
                                                                                                                                                                 Matches
                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
  FFFS
                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Maramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Makek J.A., Gunaranne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahay J., Hellon E., Ketteman M., Madan A., Rodingues S., Sanchez A.,
Miting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimmood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                             PEQUENCE OF 169-689 FROM N.A. (ISOFORM 1).

TISSUE=Placenta, and Tongue;
A Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
A Ninomiya K., Wagatsuma M., Kikkawa E., Omura Y., Abe K., Kanihara K.,
A Katsuta N., Sato K., Tanikawa M., Yamazaki M., Irie R., Sato H.,
Xamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
Kikuchi H., Murakawa K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
Kikuchi H., Murakawa K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
Kikuchi H., Murakawa K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
Kikuchi H., Wakamatsu A., Kanehori K., Sugiyama T., Otsuki T., Ishibashi T.,
Pujimori K., Masuho Y., Nagai K., Isogai T.;
NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O., "Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9NUB1-2; Sequence=VSP_007249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 336-689 FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21245130; PubMed=11347906;
                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=1
```

```
for large proteins in vitro.",
DNA Res. 8:85-95(2001).
-!- FUNCTION: Converts acetate to acetyl-CoA so that it can be used
for oxidation through the tricarboxylic cycle to produce ATP and
CO(2) (By similarity).
-!- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate +
```

acetyl-CoA.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

IsoId=Q9NUBl-1; Sequence=Displayed;

Note=No experimental confirmation available;

Lawling.

-!- CAUTION: Ref.1 (CAB81884) sequence differs from that shown due erroneous gene model prediction.

-!- CAUTION: Ref.3 sequence differs from that shown due to a frameshift in position 250 and numerous sequencing errors.

ű

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).

EMBL; AL035661; CAB75500.1; -.
EMBL; AL080312; CAB81884.1; ALT\_SEQ.
EMBL; BC039261; AAH39261.1; -.
EMBL; BC044588; AAH44588.1; -.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                               510
                                                                                                                                                                                                                                                                                                                                                                                                            68 VQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRA---EVKFEGDTLVNRIE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
-!-CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
XDb-, in which Xaa is preferably Leu, but may be other amino acids
including Pro although not Arg or Lys, and Xbb may be Pro.
-!- COFACTOR: Binds 2 manganese ions per subunit (By similarity).
-!- SUBCELIULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to peptidase family M17.
                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Last annotation update)
Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
                                                                                                                                                                                                                                                                                                                              8 FIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFSXG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDILNE=22297718; PubMed=12219091;
Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
Aksoy S.;
                                                                                                                                                                                                                                                                                                   52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRION (POTENTIAL).
ACETYL-COENZYME A SYNTHETASE 2-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Wigglesworthia.
                                      Genew; HGNC:1669; ACAS2L.
InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
PROSITE; PS00455; AMP_BINDING; 1.
Ligase; Mitochondrion; Transit peptide; Alternative splicing.
TRANSIT 36 MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                  6.7%; Score 85; DB 1; Length 689;
                                                                                                                                                                                      /FTId=VSP 007249.
V -> M (IN REF 2; AAH39261)
V -> M (IN REF 2; AAH44588)
66E84E39302AD08B CRG64;
                                                                                                                                                                                                                                                                               ; Pred. No. 15;
15; Mismatches 37; Indels
                                                                                                                                                      POLY-ALA.
Missing (in isoform 2).
/FTIG=VSP 007249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wigglesworthia glossinidia brevipalpis.
EMBL; AK027817; BABS5390.1; ALT_INIT.
EMBL; AK092295; BAC03853.1; ALT_SEQ.
EMBL; AB058749; BAB47475.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last seq
10-0CT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                    74856 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 LKGIDFKEDGNILGHKL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LAP) (Leucyl aminopeptidase).
PEPA OR WIGBR4590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  554 ------NISGHRL 560
                                                                                                                                                                                                                                                                               24.1%;
                                                                                                                                                                                                                                                                                                33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                       36
689
53
447
                                                                                                                                                                                                                                689 AA;
                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=36870;
                                                                                                                                                      446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMPA WIGBR
Q8D295;
                                                                                                                                                                                                   CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       511
                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                        DOMAIN
                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMPA_WIGBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
   à
                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

LOCALIZATION,

```
RESULT 8
      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                    YVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDF-KEDGNILGHKLEYNFISHNV 150
                                                                                                                                                                                                                                                                                                       254
                                                                                                                                                                                                                                                                                                                                         -----Y 182
                                                                                                                                                                                                                                                                                                                                                             -----SVEIMDHKKIKNIGMNAYLHVSKGSSKNPYLSIIKY
                                                                                                                                                                                                                                                                                                                                                                                  183 QONTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAA--GITHGMDEL 236
                                                                                                                                                                                                                                                                                                                                                                                                      255 NENKFNGKSPIILIGKGLTFDSGGISIKPSNNMDEMKFDMCGAAAVLGVMHAISEL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy-chain
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakateni T., Suzuki Y., Yamamoto T., Sinohara H.,
"Molecular cloning and sequencing of cDNAs encoding three heavy-cha:
precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
implications for the evolution of the inter-alpha-trypsin inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto T., Yamamoto K., Sinohara H.;
Inter-alpha-trypsin inhibitor and its related proteins in Syrian hamster urine and plasma.";
J. Blochem. 120:145-152(1996).
-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last amoctation update)
Inter-alpha-trypsin inhibitor heavy chain H3 precursor (III heavy chain H3) (Inter-alpha-inhibitor heavy chain H3) (Hcs).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                  68; Indels 49;
                                                                                                                                                   MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).

**AE181EEBEB481FE3 CRC64;
                                                                                                                                                                                                                                           DB 1; Length 501;
                                                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS.
                                                                                                                                                                                                                                                                                                                                    151 YITADKQKNGIKANFKIRHNIEDGSVQLADH-----
                                                                                                                                                                                                                                        ; Score 84.5; DB; Pred. No. 12; 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       886 AA
                          HAMMP, ME 00181, -; 1.
InterPro; IPR000819; Peptidase M17 C.
InterPro; IPR000819; Peptidase M17 N.
Pfam; PF00883; Peptidase M17, 1.
PRINTS; PR00481; ILAMNOPPIDASE.
PROSITES; PS00481; LAMNOPPIDASE.
M Hydrolase; Aminopeptidase; Manganese; Com
 to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mesocricetus auratus (Golden hamster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97420688; PubMed=9276673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97018241; PubMed=8864857;
                       EMBL; AB063522; BAC24605.1; -.
                                                                                                                                                                                                                56643 MW;
                                                                                                                                                                                                                                       6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. 122:71-82(1997).
                                                                                                                                                                                                                                                  Local Similarity 21.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                           208 YILKDKYSEKİ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heavy chain family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10036;
 send an email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITH3 MESAU
P97280;
                                                                                                                             ACT SITE
ACT SITE
METAL
                                                                                                                                                                                                                                                                                      92
                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                  METAL
                                                                                                                                                                                         METAL
                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
d
                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 LKGID--FKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 YPDHMKRHDFFKSAMPEGYVQERT----IFFKDDGNYKTRAEVKFEGD----TLVNRIE
                                                            SUBUNIT: I-alpha-I plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, bikumin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2 and bikumin, inter-alpha-like inhibitor (I-alpha-II) of H2 and bikumin, and pre-alpha-inhibitor (P-alpha-II) of H3 and bry: Heavy chains are interlinked with bikumin via a chondroitin 4-sulfate bridge to the their C-terminal aspartate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CHONDROITIN 4-SULRATE, CROSS-LINK SITE
(BY SIMILARITY).
    WHICH ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Leucyi-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bācteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Xylella.
NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine protease inhibitor; Repeat; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 886;
  HYALURONAN ROCESSES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62; Indels
                  ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC0594C6852576B8 CRC64;
SYNTHESIS AND DEGRADATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 QQNTPIGDGPVLLPDNHYLSTQSALSKDPKE 213
                                                                                                                                                                                                                  similarity).
SIMILARITY: Belongs to the ITIH family.
SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 84.5; D;
; Pred. No. 23;
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99018 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D89287; BAA13940.1; -.
InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 24.53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VWFA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00092; vwa; 1.
SMART; SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         886
439
88
577
646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              886 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leucyl-tRNA syntheta
LEUS OR XF2176.
Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         647
279
88
577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Slycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYL XYLFA
Q9PBG8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYL XYLFA
ID SYL X
ID SYL X
ID SYL X
ID COO
DT 16-OC
DT 16-OC
DT 16-OC
DT 16-OC
DT 16-OC
DT XYlel
OC Bacte
OC Math
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

```
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HI0917;
                                                                                                                                                                                                                                                                                                                                          D152 HAEIN
P44935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                       DIS2_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                       RESULT
                                                                                              유
                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 TIGKLPVPWPILVTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNY-- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 İNEQLEV-WVANFVLMAYGTGAVMAVEGHDORDQEF--ANKYGLPIROVIALKEPKNQDE 377
                                                                    ARALNE-20365777; PubMed=10910347;

KRAALNE-20365777; PubMed=10910347;

KRA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

RA Alvarengaa R., Alves L.M.C., Araya J.B., Baia G.S., Baptista C.S.,

RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Barros M.R.S.,

RA Barros M.B., Calombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

Coutinho L.L., Cristofani M., Dias-Neto B., Docena C., El-Dorry H.,

RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

RA Garnier M., Hohelsel J.D., Unnqueira M.L., Kemper E.L., Kitajima J.P.,

RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,

Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,

Marches M.V., Martins E.A.L., Martins E.M.F., Marsukuma A.Y.,

Manch C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,

Moon D.H., Nobrega F.G., Miyaki C.Y., Monteiro-Vitorello C.B.,

Nonn D.H., Nobrega F.G., Miyaki C.Y., Morteira M.A.,

Resiavoto B.R., Pereira G.S., Pereira H.A. Jr., Perquero J.B.,

A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,

Resiavoto B.R., Pereira G.S., Santelli R.V., Sawasaki H.E.,

A da Silveira J.F., Silvestri M.L.Z., Squeira W.J., de Souza A.A.,

A da Silveira J.F., Silvestri M.L.Z., Squeira W.J., de Souza A.A.,

A da Silveira J.F., Silvestri M.L.Z., Squeira W.J., de Souza A.D.,

A da Silveira J.F., Silvestri M.L.Z., Squeira W.J., de Souza A.R.,

A da Silveira J.F., Silvestri M.L.Z., Squeira W.J., de Souza A.D.,

A da Silveira J.F., Silvestri M.L.Z., Squeira W.J., de Souza A.D.,

A da Silveira J.F., Silvestri M.L.Z., Squeira W.J., de Souza A.D.,

A de Souza A.P., Terenzi M.F., Truffi D., Tsai S., Vettore A.L.,

A da Silveira J.F., Silvestri M.L.Z., Squeira W.J., de Souza A.D.,

A de Souza A.P., Terenzi M.F., Truffi D., Tsai S., Vettore A.L.,

A de Souza A.P., Van Salveira M.J., Squeira W.J., de Souza A.D.,

A de Souza A.P., Terenzi M.F., Silveira M.J., de Souza A.D.,

A de Souza A.P., Terenzi M.F., Silveira M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNFISHNVYI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAWAE, MF 00049; -; 1.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR002302; Leu-tRNAsyntla.
InterPro; IPR001302; tRNA-synt 1.
InterPro; IPR0019008; ValRS_ILERS_edit.
Pfam; PF00133; tRNA-synt_1; 1.
PRINTS; PR00985; TRNASYNTHLEU.
TIGRFAMS; TIGR00396; leuS_bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE 1; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72; Indels 55; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP + diphosphate + L-leucyl-tRNA(Leu).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 STWEPDVWRDWYADKTR---EFE---LINSAEFDGLDYQDAFEVLAERFE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "KMSKS" REGION.
ATP (BY SIMILARITY).
9FDCCB992092919E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.5%; Score 82.5; DB
20.8%; Pred. No. 33;
Live 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "HIGH" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE004031; AAF84975.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99796 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55
641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        879 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteomé.
                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
SO THE TAMES OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaisb-sib.ch).
           ---GDGPVLLPDN- 198
                                              --NTPIGDGPVL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 IFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDPKEDGNI---LGH-----KLEYNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                543 -RNLYIQSMKFKGNGIKTN-----DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Relachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKarlavage A.R., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Shilley R. Liu L. I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Finchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 19 POTENTIÁL.
20 795 PROTECTIVE SURFACE ANTIGEN D15.
795 AA; 87478 MW; B85691FC22E6ED44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - SUBCELLUTAR LOCATION: Outer membrane. -! - SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 6.5%; Score 82; DB 1; Length 795; Best Local Similarity 25.0%; Pred. No. 32; Matches 40; Conservative 22; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 SHNVYITADKQK-NGIKANFKIRHNIEDGSVQLADHYQQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 LP--DNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000184; Bac surfAg D15.
Pfam; PF01103; Bac surface Ag; I.
Antigen; Outer membrane; Signal; Complete proteome.
153 TADKQKNGIKANFKIRHNIEDGSVQLADHYQQNTPI--
                                                                                                                                                                                                                                                                                                                                                                                                                  795 AA
                                                                                                                                               199 HYLSTQSALSKDPKEKR 215
                                                                                                                                                                                             : | | : ||: 476 AFSGTGSPIKTDPEWRK 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32773; AAC22575.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 269:496-512(1995),
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
```

```
SET7_HUMAN
ID SET7_HUMAN
                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 IFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNI---LGH-----KLEYNFI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFFENYDNSKSDTSSNYKRTTYGSNVTL-GFPVNENNSYYVGLGHTYNKISNFALEYN-- 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543 -RNLYIQSMKFKGNGIKTN-----DFDFSFGMNYNSLNRGYFPTKGVKASLG-GRVT 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- NTPIGDGPVL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Minna / Serotype B, and Eagan / Serotype B;
MEDLINE=97427952; PubMed=9284140;
Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                               Flack F.S., Loosmore S., Chong P., Thomas W.R.;
"The sequencing of the 80-kDa D15 protective surface antigen of
Haemophilus influenzae.";
Gene 156:97-99(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
Haemophilus influenzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 797 PROTECTIVE SURFACE ANTIGEN D15. 797 AA; 87675 MW; 2F93DE538696AF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 797; 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: Outer membrane.
-1- SIMILARITY: Belongs to the surface antigen D15 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Indels
593 IPGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 LP--DNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 SHNVYITADKQK-NGIKANFKIRHNIEDGSVQLADHYQQ---
                                                                                                       797 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.5%; Score 82; DB 25.0%; Pred. No. 32; ative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. PROTECTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, JC4078, JC4078.
Interpro, IRR001184, Bac gurfAg_D1S.
Pfam, PF01103; Bac gurface Ag, I.
Autigen, Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invasive disease.";
Infect. Immun. 65:3701-3707(1997).
                                                                                                                                                                                                                                                                                                                                STRAIN=Serotype B;
MEDLINE=95255676; Pubmed=7737523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U13961; AAA85645.1; -.
EMBL; U60832; AAB61974.1; -.
EMBL; U60833; AAB61976.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein M.H.;
                                                                                                    D151 HAEIN
P46024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486
                  593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

```
lysine-4 specific (EC 2.1.1.43)
                                                                                                                                                                                                                                                                                                                                                          Wang H., Cao R., Xia L., Erdjument-Bromage H., Borchers C., Tempst P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., SEQUENCE OF 35-44; 108-115; 144-152; 234-258 AND 345-358, AND MUTAGENESIS OF HIS-297.
                                                                                                                                                                                                                                                                                                                                                                             Zhang Y.;
"Purification and functional characterization of a histone H3-lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21838688; PubMed=11850410; Nishloka K., Chuikov S., Sarma K., Erdjument-Bromage H., Allis C.D., Nishloka K., Chuikov S., Sarma K., Erdjument-Bromage H., Allis C.D., Tempst P., Reinberg D.; Setty a novel histone H3 methyltransferase that facilitates transcription by precluding histone tail modifications required for the terrochromatin formation."; Genes Dev. 16:479-489(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., SEQUENCE OF 36-45; 104-115; 144-152; 159-169; 201-250 AND 324-358, AND MUTAGENESIS OF HIS-297.
TISSUE=Cervical carcinoma;
                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 70-366.
MEDLINE=22401621; PubMed=12514135;
Kwon T., Chang J.H., Kwak E., Lee C.W., Joachimiak A., Kim Y.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22259601; PubMed=12372304;
Wilson J., Jing C., Walker P., Martin S., Howell S., Blackburn
Gamblin S., Xiao B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22289682; PubMed=12389038; Jacobs S.A., Harp J.M., Devarakonda S., Kim Y., Rastinejad F., Khorasanizadeh S.; "The active site of the SET domain is constructed on a knot."; Nat. Struct. Biol. 9:833-838(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.75 ANGSTROMS) OF 108-366.
MEDLINE=22459284; PubMed=12540855;
Xiao B., Jing C., Wilson J.R., Walker P.A., Vasisht N., Kelly Howell S., Taylor I.A., Blackburn G.M., Gamblin S.J.;
"Structure and catalytic mechanism of the human histone methyltransferase SET7/9.";
                                                                                                                    (SET domain-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Crystal structure and functional analysis of the histone
              QBWTS6; Q9COE6;
28-FRB-2003 (Rel. 41, Created)
28-FRB-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Histone-lysine N-methyltxansferase, H3 lysine-4 si
(Histone H3-K4 methyltxansferase, H3-K4-HWTase)
containing protein 7) (Set9) (SET7/9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 52-344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
MEDLINE=21082932; PubMed=11214970;
                                                                                                                                                                                                                                                                                                                                     MEDLINE=21638669; PubMed=11779497;
                                                                                                                                                                                                                                                                                                                                                                                                                  4-specific methyltransferase.";
Mol. Cell 8:1207-1217(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methyltransferase SET7/9.";
Cell 111:105-105(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 7:347-355 (2000).
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 421:652-656(2003)
                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                       SET7 OR KIAA1717
                                                                                                                                                                                                                                                                                                                   rissum=Brain;
```

```
NCBI_TaxID=382;
                                                                                                                                                              10-OCT-2003
                                                                                                                             RHIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                             ACS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modern by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNEDGEMTGEKLAYVYPDERTALYG----KFIDGEMIEGKL----ATLMST-EEGRPHFE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LGHK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 RYPDHMKRHDFFKSA------MPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 IMPGNSVYH-FDKSTSSCISTNALLPDPYESERV-----YVAESLISSAGEGLFSKV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                       -!-FUNCTION: Histone methyltransferase. Methylates Lys-4 of histone Histone Histone methyltransferase. Methylates Lys-4 of histone Histone Library a specific tag for epigenetic transcriptional activation.
-!-CATALYTIC ACTIVITY: S-adenosyl-L-homory tenhologyl-L-homory 6 VELDGDVNGHKFSVSGEGEGDATYGKLTLKFI---CTTGKLPVPWPTLVTTFSXGVQCFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00317; SET; 1.
PROSITE; PS50280; SET; 1.
Transferase; Methyltransferase; Chromatin regulator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005634; C:nucleus; NAS.
GO; GO:0018024; F:histone-lysine N-methyltransferase activity; NAS.
GO; GO:0016568; F:chromatin modification; NAS.
InterPro; IPR003409; MSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 LEYNFISHNVYITADKQKNG-IKANFKIRHNIEDGSVQLADHYQQNTPIGDGP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H->A,G: ABOLISHES METHYLTRANSFERASE
                                                                                                                                                                                                                                            SIMILARITY: Belongs to the histone-lysine methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.4%; Score 81; DB 1; Length 366; 22.3%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73A1217079E3BA13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Mismatches
                                                                                                                                                                                                                                                                             -!- SIMILARITY: Contains 3 MORN repeats.
-!- SIMILARITY: Contains 1 SET domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF462150; AAL69901.1; -. AB051504; BAB21808.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-PHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MORN 1.
MORN 2.
MORN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF448510; AAL56579.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 AA; 40721 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                               /9-AdoMet.";
22:292-303(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02493; MORN; 3.
Pfam; PF00856; SET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1H31; 11-NOV-02.

1MUF; 06-NOV-02.

1N6A; 04-FEB-03.

1N6C; 04-FEB-03.

1O9S; 06-FEB-03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           606594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB;
                                                                                                                                                                                                                                            1 :
                       ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 FFGVQPQIVDSDGKV-----VDGAADGN-----LCITDS----WPGQMRTV--- 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 FIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFSXG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 VQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKG
                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Acetyl-coenzyme A synthetase 2 (EC 6.2.1.1) (Acetate--COA ligase 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=1021;
MEDLINE=21396507; PubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Capela D., Barloy-Hubler F., Gouzy M., Cadieu E., Dreano S., Gloux S., Godie T., Goffeau A., Kahn D., Kies E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

-!- CARALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate +
295 ANHSFTPNCIYDMFVHPRFGPIKCIRTLRAVBADEELTVAYGYDHSPPGKSGP 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acetyl-CoA.
PTM: Acetylated. Deacetylation by the SIR2-homolog deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activates the enzyme (By similarity).
SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                      (Acyl-activating enzyme 2).
ACSA2 OR R03327 OR SMC04093.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 6.4%; Score 81; DB 1; Length 649; Local Similarity 25.0%; Pred. No. 31; hes 40; Conservative 12; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACETYLATION (BY SIMILARITY).
ACC3ED95B87BAC92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 IDFKEDG-----NILGHKL----EYNFISHNV 150
                                                                                                                                                                        649 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPRO0003; and bind.
Pfam; PF00501; AMP-binding; 1.
PRINTS; PR00154; AMPBINDING; 1.
Ligase; Acetylation; Complete proteome.
ACT SITE 517 517 517
MOD_RES 609 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL591793; CAC47906.1; -.
HAMAP; MF 01123; -: 1
                                                                                                                                                                                                                                         (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72022 MW;
                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              649 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
```

RESULT 13

```
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                    159
CONFLICT
                                                                                                                                                     Query Match
                                                                                                                                                                     Best Local
                                                                                                                                                                                  Matches
SPTTTTTTT
                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          MEDLINE=2137209; PubMed=11453916;
MEDLINE=2137209; PubMed=11453916;
MEDLINE=2137209; PubMed=11453916;
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Deterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Holtzapple B., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M., Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                   Clarke V.A., Platt N., Butters T.D., "Cloning and expression of the beta-N-acetylglucosaminidase gene from Streptococcus pneumoniae. Generation of truncated enzymes with modified adlycon specificity.", "J. Biol. Chem. 270:8805-8814(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-acetyl-D-hexosaminides.
acetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides.
-!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC DOMAIN 1.
CATALYTIC DOMAIN 2.
LPXTG SORTING SIGNAL (POTENTIAL).
AMIDE-LINKED TO CELL WALL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IRR001540; Glyco hydro 20.
InterPro; IRR001540; Glyco hydro 20.
InterPro; IRR001899; Gram pos anchor.
Pfam; PR00728; Glyco hydro 20; 1.
Pfam; PR00746; Gram pos anchor; 1.
Pfam; PR04560; YSIRK signal; 1.
TIGRFAMS; TIGR01167; LEXTG anchor; 1.
TIGRFAMS; TIGR01167; VSIRK signal; 1.
TIGRPAMS; TIGR01168; YSIRK signal; 1.
PROSITE; PS50847; GRAM POS ANCHORING; 1.
Hydrolase; Glycosidase; Cell wall; Peptidoglycan-anchor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA-N-ACETYLHEXOSAMINIDASE.
REMOVED BY SORTASE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to family 20 of glycosyl hydrolases.
                                                                                                                                Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                           28-FEB-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-N-acetylhexosaminidase precursor (EC 3.2.1.52)
           PRT; 1312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                          STRAIN=ATCC 12213;
MEDLINE=95238375; PubMed=7721787;
                                   01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, L36923; AAC41450.1; -.
EMBL, AE007923; AAC74246.1; -.
PIR, A56390; A56390.
PIR; E95006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 293:498-506(2001)
                                                                                                                  Streptococcus pneumoniae
        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33
1284
1312
616
1046
1285
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pouq
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                          NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIGR; SP0057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an amide
      STRH STRPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIMMO
```

```
13;
                                                                                                                                                                                                                                                                                                                                                               1054 NEVAANVETRPELITRTEEIPFEVIKKENPNLPAGQENIITAGVKGERTHYISVLTENGK 1113
                                                                                                                                                                                                                                                                                                                                                                                                                 101 KDDGNYKTRAEVKFEGDTLVNRIE--LKGIDFKEDGNILGHKLEYNFISHNVYITADKQK 158
                                                                                                                                                                                                                                                                                                896 NINGDWYYILGQKPEDG--GGFLKKAIENTGKTPFNQLASTKYPEVDLPTVGSMLSIWAD 953
                                                                                                                                                                                                                                                                                                                                      -----SAMP---EGYVOERTIFF--- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGIKANFKIRHNI----EDGSVQLADHYQQNTPIGDGPVLLPD-----NHYLSTQSALSK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E., Kwon-Chung K.J., Bennett J.E., "Deletion of the Candida glabrata ERG3 and ERG11 genes: effect on cell viability, cell growth, sterol composition, and antifungal susceptibility.";
                                                                                                                                                                                                                                                                ----VPWPTLVTTFSXGV-
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CP51 CANGA STANDARD; PRT; 533 AA.
P50859; Q02312;
P1-07-1996 (Rel. 34, Created)
01-07-1996 (Rel. 34, Last sequence update)
10-07-2003 (Rel. 42, Last annotation update)
24ycochrome P450 51 (RC 1.14.13.70) (CYPLI) (P450-LIA1) (Sterol 14-alpha-demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Rapid defection and identification of Candida albicans and Torulopsis (Candida) glabrata in clinical specimens by species-specific nested PCR amplification of a cytochrome P-450 lanosterol-alpha-demethylase (11A1) gene fragment.";

J. Clin. Microbiol. 32:1902-1907(1994).

-!- FUNCTION: Catalyzes C14-demethylation of lanosterol which is critical for ergosterol biosynthesis. It transforms lanosterol into 4,4'-dimethyl cholesta-8,14,24-triene-3-beta-ol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burgener-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida glabrata (Yeast) (Torulopsis glabrata).
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida.
                                                                                                                                                                                                                           78;
                                                                                                                                                                                     Score 81; DB 1; Length 1312; Pred. No. 71;
             V -> E (IN REF. 1).
Q -> E (IN REF. 1).
Q -> L (IN REF. 1).
V -> A (IN REF. 1).
E -> K (IN REF. 1).
C -> R (IN REF. 1).
V -> A (IN REF. 1).
W -> A (IN REF. 1).
W -> A (IN REF. 1).
                                                                                                                                                                                                                         36; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrob. Agents Chemother. 39:2708-2717(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1114 TTETVLDSQVTKĖVINQVVEVGAPVTHKGDĖ 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235
                                                                                                                                                                                                                                                              21 DVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 DPKEKRDHMVLLEFV----TAAGITHGMDE
 MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96161286; PubMed=8593007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95081364; PubMed=7989540;
                                                                                                                                                  144549 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 60-473 FROM N.A.
                                                                                                                                                                                                     20.7%;
                                                                                                                                                                                                                         56; Conservative
39
69
169
617
1045
1161
1171
39 3
69 6
169 16
617 61
1045 104
1161 116
1171 1177 126
                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=2001-L5;
```

```
MEDLINE=82030699; PubMed=7026551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIGRFAMB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INIT MET
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAND
TURN
HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TURN
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .09 GHEFIFNAKLADVSAEAAYSHLT-----TPV----FGKGVIYDC----PNHR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 GHKFSVS---GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFSXGV--QCFSRYPDH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MKRHDFFKSAM-PEGYV-----QERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 DFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHYQQNTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Gaps
              -!- CATALYTIC ACTIVITY: Obtusifoliol + 3 O(2) + 3 NADPH = 4-alpha-methyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate + 3 NADP(+) + 3 H(2)O.
-!- PATHWAY: Ergosterol biosynthesis.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                            EMBL; S75389; AAB32679.1; -.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PP00067; p450; 1.
PRINTS; PR00386; P450; 1.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Blectron transport; Oxidoreductase; Monooxygenase; Membrane; Heme; Sterol biosynthesis; NADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=87231095; PubNed=3473447;
Wang S.-Z., Chen J.-S., Johnson J.L.;
"Nucleotide and deduced amino acid sequences of nifD encoding the alpha-subunit of nitrogenase MoFe protein of Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1988 (Rel. 07, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrogenase molybdenum-iron protein alpha chain (EC 1.18.6.1)
(Nitrogenase component I) (Dinitrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I -> M (IN REF. 2).
I -> T (IN REF. 2).
; A0506C17507E6EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.4%; Score 80.5; DB 22.6%; Pred. No. 27; tive 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  533 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 GDGPVLLPDNHYLSTQSALSKDPKEKRD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GTYMSLIKERREKND 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 15:3935-3935(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473 473 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
01-APR-1988 (Rel. 07, Last seg
                                                                                                                                                                                                                                                                                         EMBL; L40389; AAB02329.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium pasteurianum
                                                                                                                                                                                                                                                                                                                                                                                                                                                   472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE OF 1-179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=1501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pasteurianum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLOPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P00467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLOPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIFD
SOURCE STATE STATE SOURCE COUNTY STATE STATE SOURCE COUNTY STATE STATE SOURCE COUNTY STATE STATE SOURCE SOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Hase T., Nakano T., Matsubara H., Zumft W.G.;
"Correspondence of the larger subunit of the MoFe-protein in
clostridial nitrogenase to the nif D gene products of other N2-fixing
organisms.";
J. Biochem. 90:295-298(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + 16 ATP
                                                                                                                                                                                                                                        Chen K.C.K., Chen J.-S., Johnson J.L., 
"Structural features of multiple nifH-like sequences and very biased codon usage in nitrogenase genes of Clostridium pasteurianum."; 
J. Bacteriol. 166:162-172(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88294019; PubMed=2840948;
Wang S.-Z., Chen J.-S., Johnson J.L.;
"Distinct structural features of the alpha and beta subunits of an itrogenase molybdenum-iron protein of Clostridium pasteurianum: an analysis of amino acid sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).

**MEDLINE=93344379; PubMed=8393705;

*Rim 7., Woo D., Rese D.C.;

**Aray crystal structure of the nitrogenase molybdenum-iron protein from Clostridium pasteurianum at 3.0-A resolution.";

*Biochemistry 32.7104-7115(1993).

-!- FUNCTION: The key enzymatic reactions in nitrogen fixation are catalyzed by the nitrogenase complex, which has 2 components: the iron protein and the molybdenum-iron protein.

-!- CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 AT = 8 oxidized ferredoxin + 2 NH(3) + 16 ADP + 16 phosphate.

-!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS THAT BINDS
30-32 FE, 2 MO, AND INORGANIC SULPUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00090; NITROGENASE 1 2; 1.
PROSITE; PS00699; NITROGENASE 1 1; 1.
Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-32 FE, 2 MO, AND INORGANIC SULFUR.
-!- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REF.
REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M21537; AAA83531.1; --
EMBL; Y00155; CAA68349.1; --
EMBL; M20389; AAA23265.1; --
EMBL; M20389; NICLMA,
PDB; 1MIO; 31-OCT-93.
InterPro; IPR000318; Nitrognse_compl.
InterPro; IPR000318; Nitrognse_compl.
InterPro; IPR000510; Oxred nitrognsel.
Pfam; PF00148; oxidored_nitro; 1.
                                                                                                                                                                              SEQUENCE OF 1-166 FROM N.A.
MEDLINE=86168010; PubMed=3457003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ^ ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 27:2800-2810(1988)
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 525-533 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR01282; niED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAND
TURN
STRAND
```

```
474
477
484
506
513
521
524
524
524
524
524
524
524
524
                                                                                                                                                                                                                                                                                   2212
2222
2222
2222
2222
2222
2222
2323
2323
2323
2323
2323
2323
2323
2323
2323
2323
2323
2323
2323
2323
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
233
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
233
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
233
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
233
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
233
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
233
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
233
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
233
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
2333
233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4445
4459
4464
4473
4483
4483
6509
510
510
533
743,
```

9; 17 ELDGDVNGHKFSVSGEGEGDATYGKL-------TLKFIC--TTGKLRVPW-- 57 Query Match 6.4%; Score 80.5; DB 1; Length 533; Best Local Similarity 19.9%; Pred. No. 27; Matches 48; Conservative 38; Mismatches 98; Indels 57; Gaps

ð g à

-----PTLVTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNY-KTRA 110

58

283 CNFIGVDGIVETLRDWAKCFDD-PELTKR-----TEEVIAEEIAAIQDDLDYFKEKL 333 111 EVK------FEGDTLVNRIELKGIDFKEDGNILGHKLEY-------NFISHN-- 149 150 -VYITADKOKNGIKANFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALS 208 209 K 209 454 K 454 à d à g ð g

Search completed: April 19, 2004, 15:06:28 Job time : 18 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

April 19, 2004, 15:03:20 ; Search time 20 Seconds (without alignments) 1144.679 Million cell updates/sec

US-10-057-505-2-COPY
1265
1 MSKGEELFTGVVPILVELDG......VLLEFVTAAGITHGMDELYK 238 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	green-fluorescent	hypothetical prote		_	4	oligoendopeptidase	sterol binding pro	DNA-directed DNA p	incom	inter-alpha-trypsi	hypothetical prote	DNA-binding protei	hypothetical prote	ABC-type transport	iron-regulated out	leucyl-tRNA synthe	hypothetical prote		1 28		a	polyketide synthas	glucose dehydrogen	protein F10B6 14 (	cetvl	hypothetical prote	٠,		_
	Q ·	JQ1514	H72228	D71614	AD2052	G81355	A99552	AE3629	A36028	AB3548	JC5576	B86815	T06586	F71620	E81317	H64708	E82590	H86201	T27856	JC4078	F64102	S42798	AI2140	B83911	F86281	E95006	T22410	E70390	NICLMA	C70031
	1 DB	!																											7	
	Length	238	785	2573	281	357	613	173	2222	324	883	525	632	646	564	877	887	1138	471	797	808	1092	2518	371	160	1312	322	370	534	636
%∙	Query	97.1	•	7.2	7.0	٠				٠					٠			6.5	•	•	6.5	•	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4
	Score	~~	•	91.5	œ	7	87.5	ω	'n.		4.	84	83	œ		'n	ς,	ς,	82	82	82	Φ	81.5	81	81	œ	ö	ö	80.5	Ö
	Result No.	-	7	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23		25			28	

calpain (EC 3.4.22 hypothetical prote	synaptogamin o-p65	ATP-dependent nucl	S-layer protein pr	hypothetical prote	S-adenosylmethioni	calpain (EC 3.4.22	hypothetical prote	hypothetical prote	probable exported	hypothetical prote	hypothetical prote	sensory transducti	IgA Fc receptor pr
CIHUH2 T39047	JH0414	C71633	JC4930	B32259	B97220	B24815	865213	B85362	AE1055	D71900	C72293	S75005	A60234
7 7	010	1 77	7	N	N	7	N	7	7	7	N	7	7
700	439	822	874	196	274	422	612	782	1259	400	612	661	1134
4.9	6.3	9	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.2	6.2	6.2	6.2
80.5	0 8	80	80	79.5	79.5	79.5	79.5	79.5	79.5	79	79	79	79
30	3.2	3 6	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 JQ1514  green-fluorescent protein [validated] - hydromedusa (Aequorea victoria) C;Speies: Aequorea victoria	Cylaces Us-Dec-1999 #Sequence revision Us-Dec-1999 #rext change 23-Mar-2001 Cylacession: JS0692; JQ1514; PQ0335; S48693; S51330; S51331 R/Pacsher, D.C.; Eckenrode, V.K.; Ward, W.W.; Prendergast, F.G.; Cormier, M.J. Gene 111, 229-233, 1992 A/Title: Primary structure of the Aequorea victoria green-fluorescent protein. A.Reference number: JQ1514; MUID:92175527; PMID:1347277	A; Accession: USO824 A; Molecule type: DNA A; Molecule type: DNA A; Cross-references: GB:M62654; NID:g155662; PIDN:AAA27722.1; PID:g155663 A; Accession: JQ1514 A; Molecule type: mRNA A; Residues: 1-99, FF, 101-140, L', 142-218, 'V', 220-238 <pra2> A; Cross-references: GB:M62653; NID:g155660; PIDN:AAA27721.1; PID:g155661 A; Molecule type: protein</pra2>	A, Residues: 46-64;74-122;132-151;154-183;185-200 <pra3> R, Inouye, S., Tsuli, F.1. R, Inouye, S., Tsuli, P.1. R, Inouye, S., Tsuli, P.1. R, Inouye, S., Tsuli, P.1. R, REBS Lett. 351, 211-214, 1994 A, Title: Evidence for redox forms of the Aequorea green fluorescent protein. A, Reference number: S48693; MUID:94364470; PMID:8082767 A, Accession: S48693 A, Statuus: preliminary A, Molecule type: mRNA A, Residues: 1-24, (0', 26-156, 'P', 158-171, 'K', 173-238 &lt; INO&gt; A, Residues: 10-24, (0', 26-156, 'P', 18-171, 'K', 173-238 &lt; INO&gt; A, Crose-reference (0', 20-156, 'P', 18-171, 'K', 173-238 &lt; INO&gt; A, Crose-reference (0', 20-156, 'P', 18-171, 'K', 173-238 &lt; INO&gt; A, Crose-reference (0', 20-156, 'P', 18-171, 'K', 173-238 &lt; INO&gt; A, Crose-reference (0', 20-156, 'P', 18-171, 'K', 173-238 &lt; INO&gt; A, Crose-reference (0', 20-156, 'P', 18-171, 'K', 173-238 &lt; INO&gt; A, Crose-reference (0', 20-156, 'P', 18-171, 'K', 173-238 &lt; INO&gt; A, Crose-reference (0', 20-156, 'P', 18-171, 'K', 173-238 &lt; INO&gt; A, Crose-reference (0', 20-156, 'P', 18-171, 'K', 173-238 &lt; INO&gt; A, Crose-reference (0', 20-156, 'P', 173-238 &lt; INO)&gt; A, Crose-reference (0', 20-156, 'P', 173-238 &lt; INO)&gt; A, Crose-reference (0', 20-156, 'P', 173-238 &lt; INO)&gt; A, Crose-reference (0', 20-156, 'P', 20-1</pra3>	A; Close retriences: Grillows, National 1995 A; Watkins, J.N.; Campbell, A.K. submitted to the EMBL Data Library, January 1995 A; Reference number: S51330 A; Accession: S51330 A; Molecule type: mRNA A; Residues: 1-13, 'V', 15-24, 'Q', 26-44, 'N', 46-153, 'G', 155-156, 'P', 158-171, 'K', 173-227, 'R', A; Cross-references: EMBL: X83959; NID:g634008; PIDN: CAA58789.1; PID:g634009 A; Experimental source: clone gfpl A; Accession: S51331	A; Molecule type: mRNA A; Residues: 1-24, 'Q', 26-29, 'R', 31-83, 'L', 85-153, 'G', 155-156, 'P', 158-171, 'K', 173-208, 'Q', A; Cross-references: EMBL: X83960; NID: 9634010; PIDN: CRAS8790.1; PID: 9634011 A; Experimental source: clone gfp2 B; Experimental source: clone gfp2 R; Yang, F:, Moss, L.G.; Phillips Jr., G.N. submitted to the Brookhaven Protein Data Bank, August 1996 A; Reference number: A65692; PDB: 1GFL A; Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 'A', 2-79,'R', 81-5, A; Mots: angineered sequence based on J01514, cloned and expressed in Escherichia coli R; Yang, F:, Moss, L.G.; Phillips Jr., G.N. Nat. Biotechnol: 14, 1246-1251, 1996 A; Title: The molecular structure of green fluorescent protein.
--	---	--	---	---	--

```
| :||:|
237 TYLKRERDYM 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 KDPKEKRDHM 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: PFB0460c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: all1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Residues: 1-785 <ARN>
A,Cross-references: GB:AE001806; GB:AE000512; NID:G4962196; PIDN:AAD36691.1; PID:G498219
A,Experimental source: strain MSB8
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: H72228
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
A, Contents: annotation, X-ray crystallography, 1.9 angstroms (c) comment: This protein is excited by the photoprotein aequorin (see PIR. AQJFNV) emittin C; Comment: The chromophore of this protein is formed by modification of Ser-dehydro-Tyr-C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 399, 323-329, 1999
A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A,Reference number: A72200; MUID:99287316; PMID:10360571
A,Accession: H72228
                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 TIFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 RIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VITESYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFYKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NRIELKGIDFKEDGNILGHKMEYNYSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NRIBLKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKKDHMILLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LVRKGLLPHPYVGM-
                                                                                                                                                                                                                                                                                                                                                                                              1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                  1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60;
                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                   A; Introns: 69/3; 167/3
C;Superfamily: green-fluorescent protein
C;Keywords: chromoprotein; luminescence
C;Keywords: chromoprotein; luminescence
F;65-67/Cxoss-link: 5-imidazolinone (Ser-Gly) #status experimental
F;65/Modified site: dehydrotyrosine (Tyr) #status experimental
                                                                                                                                                                                                                                                                     97.1%; Score 1228; DB 1; Length 238;
llarity 95.8%; Pred. No. 5e-98;
Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.6%; Score 96; DB 2; Length 785; Best Local Similarity 20.9%; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein TM1624 - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 NEGRESFEGTVPGVVQAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 YQQNTPIGDGP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEONYGVLGGP 145
                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 228; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: TM1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                     Query Match
                                                                                                    A;Gene: GFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

```
Gispecies: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AD2052

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans A;Reference number: AB1807; MUID:21595285; PMID:11759840
hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum)
CjSpecies: Plasmodium falciparum
CjSpecies: Plasmodium falciparum
CjSates: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
CjAccession: D71614
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Fertees, M.; Salzbergy, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                         A; Accession: D71614
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-2573 cGAR>
A; Residues: 1-2573 cGAR>
A; Residues: 1-2573 cGAR>
A; Residues: 1-2573 cGAR>
A; Experimental source: clone 3D7
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA*
A;Residues: 1-281 «CMD»
A;Crosa-references: GB:BA000019; PIDN:BAB73669.1; PID:g17131060; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 YKTRAEVKFEGDTLVNRIELKGI----DFKEDGNILGHKLEYNFISHNVYITADKQKNGI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 KANFKI--RHNIEDGSVQLADH-----YQQNTPIGDG---PVLLPDNHYLSTQSALSK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 FKARS-LQSSSDILLNPIKYNNLQNRPDWKKDEYYIVHAEGYKY-KHE----SSKRKHSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 VOERTIFFKD--DGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNFISH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVYITADKOKNGIKANFKIRHNIEDGSVOLADHYQONTPIGDGPVLLPDNHYLSTOSALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein all1970 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 2573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.0%; Score 88; DB 2; Length 281; Best Local Similarity 25.2%; Pred. No. 4.5; Matches 34; Conservative 27; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.2%; Score 91.5; D
Best Local Similarity 26.9%; Pred. No. 41;
Matches 35; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 DPKEKRDHMVLLEFV 224
```

ო

```
ALSEOLUE BARACHEE BONA polymerase (EC 2.7.7.7) II catalytic chain - yeast (Saccharomyces cere)

DNA-directed DNA polymerase (EC 2.7.7.7) II catalytic chain - yeast (Saccharomyces cere)

Alfernate names: DNA-directed DNA polymerase II chain A; protein N0825; protein YNL26.

C.Species: Saccharomyces cerevisiae

C.Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 21-Jul-2000

C.Accession. A36028, B36029; S63235; S65121

R.Morrison, A.; Araki, H.; Clark, A.B.; Hamatake, R.K.; Sugino, A.

A,Fitle: A third essential DNA polymerase in Saccharomyces cerevisiae.

A,Reference number: A36028, MUID:90381771; PMID:2169349

A,Accession: A36028

A,Accession: B36028

A,Accession: B36028

A,Accession: B36028

A,Accession: B36028

A,Accession: B36028

A,Accession: B36028

A,Residues: 1-2222 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >
A,Fesidues: 1-2221 <AMOR >

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sterol binding protein [imported] - Brucella melitensis (strain 16M)

(Species: Brucella melitensis

C;Species: Brucella melitensis

C;Accession: AE3629

(ASCESSION: AE3629

(ASCESSION: AE3629

(ASTELVECTION: A.) Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, B.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes: Proc. Natl. Acad. Scl. U.S.A. 99, 443-448, 2002

A;Aftle: The genome sequence of the facultative intracellular pathogen Brucella meliten: A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FFSRDITVTGD-----MEAMLALRNALDDCNVDLPADLGNG 140
         ---KDPKEKRDHMVLLEFVTAAG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 KGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIXANFKIRHNIEDGSVQL-ADHYQQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Crose-references: GB:AE008918; PIDN:AAL54200.1; PID:g17985169; GSPDB:GN00191
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 FSRYPDHM-KRHDFFKSAMPEGYVQE----RTIFFKDDGNYKTRAEVKFEGDTLVNRIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 FERLGEHVNKRRGFRPSDLPFTFLVEPGKPRISVFRQDAAFE--ADAAIEGPLVMLLALL
                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.9%; Score 87; DB 2; Length 175; 26.8%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 AGPF--GPVVRSIAGYI-REKALGADAHDREAH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 NTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDH 217
         177 QLADHYQQNTPIGDGPVLLPDNHYLSTQSALS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity 26.8
41; Conservative
                                                                                                                                                                                   229 ITHGMDELYK 238
                                                                                                                                                                                                                                                :: | |||||
163 VSRGNIELYK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 EG---KLDGDAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule_type: DNA
A;Residues: 1-173 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: BMEII0958
A;Map position: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE3629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                d
                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                    C,Accession: G81355
R; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.; Vandull, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A91250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A99552
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-357 <PAR>
A, Cross-references: GB:AL139076, GB:AL111168, NID:g6968128, PIDN:CAB73096.1, PID:g696827
A, Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                       Campylobacter jeju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| :: || || || || 33 || 133 || 14 || 14 || 14 || 15 || 14 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 SYLESLKLEEDFNILNNKI-INYISNNISVNVVDSHFREISQKFEFMYYSFFNQIGDENQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 KRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKF--EGDTLV-----NRIELKG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GNILGHKL---EYNFISHNVYITADKQKN--GIKANFKI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AL445566; PID:914089735; PIDN:CAC13494.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LKGIDFKEDGNILGHKLEYNFISHNVYI-TADKQKNGIKANFKIRH-----NIEDGSV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
                                                                                                                                                                                                                                                                        C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :: :: | | : | : | : | | SKEIKEYKKYSDVPKEYRFDLDYLLEGKTIDQLF---DQFLEKSKKLIKIK-DSKYONIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 EKHSFIKKYFKEFYTKDFKLFASKDKHYRTRAELSFYHENDTLFYAMFDPKSKKKYIIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligoendopeptidase f [imported] - Mycoplasma pulmonis (strain UAB CTIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                              Cj0831c [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Keywords: methyltransferase; S-adenosylmethionine
                                                                                                                                                                                                                              tRNA (uracil-5-)-methyltransferase (EC 2.1.1.35)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.9%; Score 87.5; DI
26.6%; Pred. No. 6.8;
ive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.9%; Score 87.5; Di
22.6%; Pred. No. 14;
:ive 38; Mismatches
    QQKEKLSQDKIQELV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 22.61
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-613 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 IDFKED--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 RHNI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 LSNI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: trmA; Cj0831c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: G81355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: MYPU 3210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            쉱
엄
```

6

95

```
inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
C;Accession: dC5576; PC4486
R;Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.
A;Title: Molecular 122, 71-82, 1997
A;Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors sin inhibitor heavy chain family.
A;Reference number: dC5574; MUID:97420688; PMID:9276673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 34-53;449-475;509-526 <NA2>
C;Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 welthat: In the plasma three inter-alpha-trypsin cancer.
C;Comment: In the plasma three internal comportant role of panceatic cancer.
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
F;236-239,664-865/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.; Ehrl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein ypgD [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C,Species: Lactococcus lactis subsp. lactis C,Species: Lactococcus lactis subsp. lactis C,Sacession: B86815 C;Accession: B86815 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl: R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl: A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s: A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 LKGID--FKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADHY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- 137
                                                                                                                     131 FAPKG--QRLAIARYNGATLIWAGTAAKPVELEWKGAHIGITFSPDGRFLITSMQENALH 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 YPDHMKRHDFFKSAMPEGYVQERT----IFFKDDGNYKTRAEVKFEGD----TLVNRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
78 VTELANIPRKWITAVATGPNGTVGFASGKTAWSRAADG-KVQEFTQERSVEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 84; DB 2; Length 529; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | :::: | | | 593 HFVTPLTPMVVTKPEDN--EDQTSIADKPGE 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 QONTPIGDGPVLLPDNHYLSTQSALSKDPKE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.7%; Score 84.5; D
Best Local Similarity 24.5%; Pred. No. 41;
Matches 37; Conservative 33; Mismatches
                                                                100 FKDDGNYKTRAEVKFEGDTLV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: mRNA
A,Residues: 1-889 <NAK>
A,Cross-references: DDBJ:D89287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: liver A; Accession: PC4486
                                                                                                                                                                                                                                       189 GWRLEDN 195
                                                                                                                                                                                138 GHKLEYN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: B86815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: JC5576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: ypgD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      장 임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                    ద
                                                                                                                  셤
                                                                                                                                                                                à
                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                               A; Molecule type: DNA
A; Residues: 1-222 <SENA
A; Cross-references: BMBL:21538; NID:g1302316; FIDN:CAA96169.1; PID:g1302317; GSPDB:GNOC
A; Experimental source: strain S288C
R; Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
A; Sest. Tobe sequence of a 24 152 bp segment from the left arm of chromosome XIV from Sa
A; Reference number: S65111; MUID:96310631; PMID:8740425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vegetatible incompatibility protein het-e-1 [imported] - Brucella melitensis (strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Residues: 1-2221 <SEF>
A)Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63235.1; PID:g1045247
A)Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61; Indels 59; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      943 FFEVDGPYKAMILPSSKEEGKGIKKRYAVFNEDGSLAELKGFELKRRGEL---QLIKNFO 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPKSFPETYFFTLENGKKLYLSYPCSMLNYRVHQKFTNHQYQELKDPLNYIYETHSENTI 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---IELKGIDFKEDGNILGHKLEYNFI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: AE008918; PIDN: AAL53549.1; PID: g17984458; GSPDB: GN00191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIGGIPFFAMADGAVHRLDDGHQTSTVHDGLLSAAMAVDGKSLVTGGEDGRVCRIDAKGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---VSGE----GEGDATYGKLTLKFI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AB3548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CT-TGKLPVPWPTLVTT----FSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---KRHDFFKSAMPEGYV----QERTI
   R;Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H. submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: SGD:S0005206; MIPS:YNL262w
A;Map position: 14L
C;Superfamily: DNA-directed DNA polymerase II
C;Superfamily: DNA binding; nucleotidyltransferase; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.8%; Score 85.5; DB 1; Length 2222; Best Local Similarity 28.2%; Pred. No. 1.1e+02; Matches 37; Conservative 13; Mismatches 50; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 324;
                                                                                                                                                                                                                                                                                                                                             A; Accession: S65121
A; Status: mucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 84.5; D; Pred. No. 11; 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPVPWP-TLVTTFSXGVQCFSRYPDHM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 FTGVVPILVELDGDV----NGHKFS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FFKDDGNYKTR--AEVKFEGDTLVNR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SGD: POL2; DUN2; MIPS: YNL262w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDIFKVFLEGD 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.73
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 S--HNVYITAD 155
                                                                A, Reference number: S63235
A, Accession: S63235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Residues: 1-324 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
Gene: BMEII0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ПP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

à

ä

φ ••

146

172

120

```
A;Residues: 1-564 <PRA.
A;Residues: 1-564 <PRA.
A;Cross-references: GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73385.1; PID:g696856
A;Cross-references: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: wlaB; Cj1130c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillir C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Cawure 403, 655-669, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; WUID:20150912; PMID:10688204
                                                                         GB:AE001362; NID:93845124; PIDN:AAC71835.1; PID:9384512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABC-type transport protein Cj1130c [imported] - Campylobacter jejuni (strain NCTC 11168)
                                                                                                                                                                                                                                                                                                                 460 NAEVKKKKNTLRKKKKKEKKNFLNDHMKEVTKNDDDDDDDDDDDDDDDNMTKVEEKOKYNDE 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYVQERTIFFKDDGNYKTRAEVKFEGD-----TLVNRIELKGIDFKEDGNILGHKLEYN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYEGKKYLFKNINLNIKKGEKIAFIGESGCGKSTLVDLI--IGLLKPKEGQILIDEQELN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGKENVSIDNVEECNKMKDEYDKKENNVSNIEEENIILDSKEQNIILDTNKEKLISKEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 -----FISHNVYITADKQKNGI-----KANFKIRH-NIEDGSVQLADHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --QLADHYQQN----TPIGDGPVLL---PDNHYLST--QSALSKDPK
                                                                                                                                                                                                                                                                                   QERTIFFKDDGN--YKTRAB--VKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNFI---
                                                                                                                                                                                                                                                                                                                                                                              ----SHNVYITA-----DKOKNGIKANFKIRHNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQNTP-----IGDGPVLLP--DNHYLSTQSALSKOPKEKRDHMVLLEFVTAAGITHG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iron-regulated outer membrane protein - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55;
                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Indels
                                                                                                                                                                                       Length 646;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                     50;
                                                                                                                                                                                       6.6%; Score 83; DB 2;
22.4%; Pred. No. 36;
cive 30; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.5%; Score 82.5; DE
25.0%; Pred. No. 33;
cive 29; Mismatches
                                                                      A;Cross-references: GB:AE001381;
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0230c
                                                                                                                                                                                       Query Match
Best Local Similarity 22.4%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 25.0%
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --MDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  522 KIMDELYK 529
  A;Status: preliminary; 1
A;Molecule type: DNA
A;Residues: 1-646 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGSV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 EKR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         580 KKK 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: E81317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: E81317
                                                                                                                                                                                                                                                                                   94
                                                                                                                                                                                                                                                                                                                                                                              147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Pisum sativum (garden pea)
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T06586
R;Sato, N.; Kazuno, A.A.; Ohta, N.; Ohshima, K.
submitted to the EMBL Data Library, June 1996
A;Bescription: Identification of a novel family of DNA-binding proteins with two AT-hook
A;Reference number: Z15774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: F71620
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A1600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
  13;
                                                                                                                                        110
                                                                                                                                                                     319 AFESKLELKNLAVAFPDGQ-----KIEYPEIVIEKGKKYAIIGDSGSGKSTLINLLVGN 372
                                                                                                                                                                                                                                                           408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --YNFISHNVYITADKOK----N 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 LKGIEPTDNSTLLDEKFENALGNKILKEISNPRHDVESANHSTHNKQVTVSHQKAIETNN 527
                                                                                     266 GVVMSVGNLSGTVTNYSKSVANSLILLNATGKLLEKYGKITDESKVTDGE-----EVT 318
                                                                                                                                                                                                                                111 EVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHN 170
                                                                                                                                                                                                                                                                                                                        171 IEDGSVQLA-----DHYQQNTP-----IGDGPVLLPDNHYLS---- 202
                                                                                                                                                                                                                                                                                                                                                          | | | | :::|
427 IFDKSIRIACADDFVFNKLDTVYDKNLSGGQQERLSVARELMGSKPILVMDESTASVDKK 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 PDHMKRHDFFKSAMPEGYV------QERTIFFKDDGNYKTRAEVKFEGDTLVNRIE 124
                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 LVELDGDVNGHKFSVSGEGBGDATYGKLTLKFICTTGKLPVPWPTLVTTFSXGVQCFSRY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-Dinding protein PD2 - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
                                                                                                                                   63 TFSXGVQCFS---RYPDHMKRHDFFKSAMPEGYVQ--ERTIFFKDDGNYKTRA-----
                                         10 GVVPILVELDGDVNGHKFSVSGE-----GEGDATYGKLTLKFICTTGKLPVPWPTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:X98740; NID:e995229; PIDN:CAA67292.1; PID:e275185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein PFB0230c - malaria parasite (Plasmodium falciparum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
  74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.6%; Score 83; DB 2; Length 632; 23.3%; Pred. No. 35; tive 23; Mismatches 82; Indele
  Indels
  : 96
                                                                                                                                                                                                                                                                                                                                                                                                                  203 TOSALSKDPKEKRDHMVLLEFVTAAGITHGM-DE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  528 QSQVEDVAKKNIQDDSKPSEESLHKADKYR 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 GIKANFKIRHNIEDG-----SVQLADHYQ 183
  43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: cv. Alaska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 LKGIDFKEDGNILGHKLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.3$
Matches 49; Conservative
  61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-632 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: F71620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                487
Matches
                                                                                  g
                                                                                                                                 ö
                                                                                                                                                                             Б
                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               집
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
```

10;

C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 29-Sep-1999
C;Accession: H64708
R;Tonc, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
R; Paperson, S.; Loftus, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; Reference number: A64520; MUID:97394467; PMID:9252185
A; Recession: H64708
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Mesedues: 1-877 < TOM>A; Residues: 1-877 < TOM>A; Residues: 1-877 < TOM>A; Complete type: DNA
A; Com

Query Match
6.5%; Score 82.5; DB 2; Length 877;
Best Local Similarity 35.3%; Pred. No. 59;
Matches 36; Conservative 7; Mismatches 26; Indels 33; Gaps

115 EGDTLVNRIEL--KGIDFK-----EDGNILGHKLEYNFISHN--VYITADKQKNGIKAN 164 

dd ð d

à

165 FKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSA 206 

Search completed: April 19, 2004, 15:07:59 Job time: 21 secs

```
April 19, 2004, 15:07:31; Search time 47 Seconds (without alignments) 1395.962 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                               ......VLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1124875 segs, 275673149 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLÓSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                 US-10-057-505-2-COPY
1265
1 MSKGEELFTGVVPILVELDG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                         Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### CITAMATO

	Description	Sequence 52, Appl	Sequence 76, Appl	Sequence 54, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 74, Appl	Sequence 87, Appl	Sequence 87, Appl	Sequence 4, Appli	Sequence 1, Appli	Sequence 125, App
	ID	US-10-214-932-52	US-10-214-932-76	US-10-214-932-54	US-09-884-681-2	US-09-967-301-2	US-10-457-982-2	US-10-024-686-2	US-10-057-505-2	US-10-293-580-2	US-10-293-580-74	US-09-927-876-87	US-10-360-149-87	US-09-920-922-4	US-09-852-000-1	US-09-900-345A-125
	E E	14	14	14	9	10	12	13	13	14	14	11	15	9	6	10
	Query Match Length DB	545	548	1192	238	238	238	238	238	238	238	387	387	238	238	238
,e	Query Match	98.0	98.0	0.86	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.6	97.6	97.5	97.5	97.5
	Score	1240	1240	1240	1238	1238	1238	1238	1238	1238	1238	1235	1235	1234	1234	1234
	Result No.		7	٣	4	Ŋ	9	7	80	σ	10	11	12	13	14	15

Sequence 2, Appli	7	ď	8	10	ģ	10,	159	10,	13	'n	'n	Sequence 53, Appl	Sequence 2, Appli	Sequence 2, Appli	7	Sequence 3, Appli	9	Sequence 62, Appl	Sequence 64, Appl	9	Sequence 68, Appl	Sequence 70, Appl	Sequence 94, Appl	Sequence 96, Appl	98,	100	102,	Sequence 104, App	
US-09-866-538-2	US-09-794-308-2	US-09-865-291-2	US-10-132-067-8	US-10-121-258-10	US-10-221-461-6	US-10-305-765-10	US-10-305-765-159	US-10-305-633-10	US-10-305-633-159	US-10-370-570-1	US-10-370-570-3	US-10-370-570-53	US-09-899-954B-2	US-10-370-570-2	US-10-132-067-2	US-10-442-148A-3	US-09-900-345A-60	US-09-900-345A-62	US-09-900-345A-64	US-09-900-345A-66	US-09-900-345A-68	US-09-900-345A-70	US-10-305-765-94	US-10-305-765-96	US-10-305-765-98	US-10-305-765-100	US-10-305-765-102	10-30	US-10-305-765-110
10	10	10	17	14	14	14	14	14	14	15	15	15	σ	15	12	15	10	10	10	10	10	10	14	14	14	14	14	14	14
238	238	238	238	238	238	238	238	238	238	238	238	238	238	238	238	239	243	243	243	243	243	243	243	243	243	243	243	243	243
97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.3	97.3	97.3	97.3	97.3	97.3	97.3	97.3	97.3	97.3	97.3	97.3	97.3	97.3	97.3
1234	1234	1234	1234	1234	1234	1234	1234	1234	1234	1234	1234	1234	1233	1233	1231	1231	1231	1231	1231	1231	1231	1231	1231	1231	1231	1231	1231	1231	1231
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VTTPSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPTL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 98.0%; Score 1240; DB 14; Length 545; Best Local Similarity 97.9%; Pred. No. 4e-124; Matches 233; Conservative 1; Mismatches 4; Indels 0
Sequence 52, Application US/10214932
PUblication No. US20030100707A1
GENERAL INFORMATION:
APPLICANT: HARNG, Inhwan
APPLICANT: KIM, Dae Heon
APPLICANT: LEE, Yong Jik
ITTLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
FILE REPERENCE: APP02/US
CURRENT APPLICATION NUMBER: US/10/214,932
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic Sequence US-10-214-932-52
                                                                                                                                                                                                                                                                                        SEQ ID NO 52
LENGTH: 545
TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           상 원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽
```

```
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                 \delta
                                                                                                 à
                                                                                                                                      셤
                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 MSKGEELFTGVVPILVELDGDVNGHKRSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTISFKDDGNYKTRAEVKFEGDTLV 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYQQNTPIGDGFVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                       488 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITHGMDELYK 545
181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1240; DB 14; Length 1192;
Pred. No. 1.2e-123;
1; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                  Sequence 76. Application US/10214932
Publication No. US200301007071
GENERAL INFORMATION:
APPLICANT: HWANG, Inhwan
APPLICANT: KIM, Dae Heon
APPLICANT: LEE, Yong Jik
TILE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
FILE REFERENCE: APPLICATION NUMBER: US/10/214,932
CURRENT APPLICATION NUMBER: US/200-08-08
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 98.0%; Score 1240; DB 14; Best Local Similarity 97.9%; Pred. No. 4e-124; Matches 233; Conservative 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HWANG, Inhwan
APPLICANT: HWANG, Inhwan
APPLICANT: KIM, Dae Heon
APPLICANT: LEE, YONG JİK
TILLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
FILE REFERENCE: APB02/US
CURRENT APPLICATION NUMBER: US/10/214,932
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-214-932-54
; Sequence 54, Application US/10214932
; Publication No. US20030100707A1
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 97.9
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 54
LENGTH: 1192
                                                                                                   SULT 2
-10-214-932-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORM
US-10-214-932-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-214-932-76
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 76
LENGTH: 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                    g
  ò
```

```
ö
                                                                                                                                                                                                                         955 MSKGEELFTGVVPILVELDGDVNGHKFSVSGBGBGDATYGKLTLKFICTTGKLPVPWPTL 1014
                                                                                                                                       1015 VITESYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTISFKDDGNYKTRAEVKFEGDTLV 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                            121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                             61 VITIESKGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cubitt, Andrew B.
TITLE OF INVENTION: Assays for Protein Kinases Using Fluorescent Protein Substrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOEDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.9%; Score 1238; DB 9;
Best Local Similarity 97.5%; Pred. No. 2e-124;
Matches 232; Conservative 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION UNBER: 08/679,865

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John 2, PRESISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 02307Z-069000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/884,681
APPLICATION NUMBER: US/09/884,681
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Tinear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-884-681-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-884-681-2; Sequence 2, Application US/02884681; Patent No. US20020061546A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tsien, Roger Y. Cubitt, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
```

```
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-024-686-2
                                                                                                                                              US-10-457-982-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                         심
                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                   임
                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                      121 NRIELKGIDFKEDGNILGHKLEYNYNSHNYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVOLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVOLAD 180
VTTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                    121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKIRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 60
                                                                                                                  181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                          181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Trien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Liopis, Juan
APPLICANT: Liopis, Juan
APPLICANT: Remington, S. James
ITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
ITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
FILE REFERENCE: 07257/071001
CURRENT APPLICATION NUMBER: US/10/457,982
CURRENT FLING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/172,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1238; DB 10;
Pred. No. 2e-124;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                        CURREAL INFORMATION:
APPLICANT: Stubbs, Simon L.
APPLICANT: Jones, Anne E.
APPLICANT: Michael, Nigel P.
APPLICANT: Michael, Nigel P.
APPLICANT: Thomas, Nicholas
TITLE OF INVENTION: Fluorescent Proteins
FILE REFERENCE: PA0111
CURRENT APPLICATION NUMBER: US/09/967,301
CURRENT FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2:
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10457982
Publication No. US20030212265A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                            Sequence 2, Application US/09967301
Publication No. US20030175859A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.5%;
Matches 232; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Aequorea victoria
US-09-967-301-2
                                                                                                                                                                                                                                   US-09-967-301-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-457-982-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                        gg
                                                                                                                  à
                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VITIFSYGVOCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                     1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLILKFICTTGKLPVPWPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                    1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                            Score 1238; DB 12; Length 238;
Pred. No. 2e-124;
1; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10024686
Publication No. US20020123113A1
GENERAL INFORMATION:
APPLICANT: Tien, Roger Y.
Heim, Roger
TITLE OF INVENTION: MODIFIED GREEN FLUORESCENT PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: Windiws95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/024,686
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/057,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 07257/032002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ADARDOMS

PILING DATE: ADARDOMS

FILING DATE: 10-OCT-1996

APPLICATION NUMBER: 085/14692

FILING DATE: 13-NOV-1995

FILING DATE: 10-NOV-1995

FILING DATE: 10-NOV-1994
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 38
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Haile, Lisa A. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 619/678-5099
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.5%;
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2
                                                                                                                                 TYPE: PRT
ORGANISM: Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: La Jolla
```

TYPE: amino acid

```
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                     61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                61 VITESYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                                                                                                         NRIELKGIDFKEDGNILGHKLEYNFISHNYYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                    VTTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NRIELKGIDEKEDGNILGHKLEYNYNSHNYYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VITESYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSKGBELFTGVVPILVELDGDVNGHKRSVSGECEGDATYGKLTLKFICTTGKLPVFWPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMYLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                    1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                    1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                ;
0
                                                                                                                                       DB 13; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.9%; Score 1238; DB 13; Length 238; Best Local Similarity 97.5%; Pred. No. 2e-124; Matches 232; Conservative 1; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGET
APPLICANT: HIM, ROGET
APPLICANT: HIM, ROGET
APPLICANT: CUBITT, Andrew
TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
FILE REFERENCE: REGENIA260-3
CURRENT APPLICATION NUMBER: US/10/057,505
CURRENT APPLICATION NUMBER: US 08/792,553
PRIOR APPLICATION NUMBER: US 08/792,553
PRIOR APPLICATION NUMBER: US 09/396,003
PRIOR APPLICATION NUMBER: US 09/396,003
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PARENTIN VERSION 3.1
SEQ ID NO 2
LENGTH: 238
                                                                                                                                                                              5; Indels
                                                                                                                              Query Match 97.9%; Score 1238; DB 13
Best Local Similarity 97.5%; Pred. No. 2e-124;
Matches 232; Conservative 1; Mismatches 5
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10057505
Publication No. US20020164674A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Aequorea victoria
US-10-057-505-2
                                                                        ,
US-10-024-686-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-057-505-2
                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           дa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
US-10-293-580-2
Sequence 2, Application US/10293580
Sequence 2, Application US/10293580
Sequence 2, Application US/10293580
Sequence 2, Application US/10293580
Sequence 2, Application US/1029380
GENERAL INFORMATION:
TOTAL OF INVENTION: Fluorescent froncein Sensors of Post-Translational Modifications
TILE OF INVENTION: Pluorescent Protein Sensors of Post-Translational Modifications
FILE REPERENCE: AURGOL OF 11-12
CURRENT APPLICATION NUMBER: US/10/293,580
CURRENT APPLICATION NUMBER: US/99/129,192
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 74, Application US/10293580
Publication No. US20030170767A1
GENERAL INFORMATION:
APPLICANT: Aurora Biosciences Corporation
APPLICANT: Cubitt, Andrew B.
TITLE OF INFORMATION: Fluorescent Protein Sensors of Post-Translational Modifications
TITLE OF INFORMATION: Ridorescent Protein Sensors of Post-Translational Modifications
TITLE OF INFORMATION: US/05/10293,580
CURRENT APPLICATION NUMBER: US/10/293,580
CURRENT APPLICATION NUMBER: US/09/1129,192
PRIOR APPLICATION NUMBER: US/09/129,192
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 74
LIBRICH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VITFSXGVQCFSRYPDHMRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VITESYGVQCFSRYPDHMKRHDFFKSAMPBGYVQERIIFFKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NRIBLKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSKGBELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Aequorea green fluorescent protein phosphorylation mutant US-10-293-580-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.9%; Score 1238; DB 14; Length 238; Best Local Similarity 97.5%; Pred. No. 2e-124; Matches 232; Conservative 1; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1238; DB 14; Length 238;
Pred. No. 2e-124;
1; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.9%;
Best Local Similarity 97.5%;
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Aequorea
US-10-293-580-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-293-580-74
```

ö,

g

à g

ò

```
121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLV 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 TTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTISFKDDGNYKTRAEVKFEGDTLVN 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 RIELKGIDFKEDGNILGHKLEYNYNSHNVYITADKQKNGIKANFKIRHNIEDGSVQLADH 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VITESYGVOCESRYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 TTFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFPKDDGNYKTRAEVKFEGDTLVN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPMPTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 YQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 YQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWYLLEFVTAAGITHGMDELYK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein US-10-360-149-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.6%; Score 1235; DB 15; Length 387; 97.9%; Pred. No. 8.4e-124; Live 1; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.5%; Score 1234; DB 9;
97.1%; Pred. No. 5.3e-124;
iive 2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09920922;
Parent No. US20020083488A1
GENERAL INFORMATION:
APPLICANT: MAYWAKI, Atsushi
APPLICANT: MAYWAKI, Atsushi
APPLICANT: Sawano, Asako
TITLE REPERENCE: 11283-012001
GURRENT APPLICATION NUMBER: US/09/920,922
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: UP 2000-237166
PRIOR PILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FRASEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 238
PRIOR APPLICATION NUMBER: US/09/927,876
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/225,035
PRIOR FILING DATE: 2000-08-11
PRIOR PELING DATE: 2000-08-11
PRIOR PLING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 107
SEQ ID NO 87
: EDWING TO NOS: 107
SEQ ID NO 87
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Aequorea victoria
US-09-920-922-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 97.9
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.5
Best Local Similarity 97.1
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-920-922-4
                                                                                                                                                                                                                                                                                                 LENGTH: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ПP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ENTAILOR.
APPLICANT: Campbell, Robert K
APPLICANT: Campbell, Robert K
APPLICANT: Campbell, Robert K
APPLICANT: Kelton, Christie A
APPLICANT: He, Chaomei
TITLE OF INVENTION: No. US20040005554Alel Glycoproteins and Methods of Use Thereof
FILE REFERENCE: 2093-003
FILE REFERENCE: 2093-003
CURRENT FPLILA DATE: 2001-08-10
PRIOR PELLOR OATE: 2000-08-11
PRIOR PLILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEC ID NOS: 107
SEC ID NOS: 107
SEC ID NO 87
LENGTH: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: El Tayar, Nabil
APPLICANT: El Tayar, Nabil
APPLICANT: Campbell, Robert K
APPLICANT: Kelton, Christie A
APPLICANT: He, Chaomei Transporteins and Methods of Use Thereof
TITLE OF INVENTION: No. US20030219786Alel Glycoproteins and Methods of Use Thereof
FILE REFERENCE: 20993-003
CURRENT APPLICATION NUMBER: US/10/360,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 TTFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTISFKDDGNYKTRAEVKFEGDTLVN 270
                                                     61 VITFSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                  NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                              62 TIPSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 RIELKGIDFKEDGNILGHKLEYNFISHNVYITADKQKNGIKANFKIRHNIEDGSVQLADH 181
                            VITFSKGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                        HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                          182 YQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 YQONTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDELYK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1235; DB 11;
Pred. No. 8.4e-124;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 87, Application US/09927876; Publication No. US20040005554A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-360-149-87

Sequence 87, Application US/10360149

; Publication No. US20030219786A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 97.9%;
Matches 232; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-927-876-87
                                                                                                                                  121
                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
```

qq à g ŏ 유

В à ö

```
업
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 125, Application US/09900345A
Publication No. US20030031999A1
GENERAL INFORMATION:
APPLICANT: Zhou, Jian Hector
APPLICANT: Zhou, Jian Hector
TITLE OF INVENTION: EFFICIENCY OF A CODON
TITLE OF INVENTION: EFFICIENCY OF A CODON
TITLE OF INVENTION: APPLICATION NUMBER: US/09/900,345A
CURRENT APPLICATION NUMBER: US/09/900,345A
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: PCT/AU00/00008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VITFSXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VITFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
121 NRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLBFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                 1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Osumi, Takashi
APPLICANT: Tsukamoto, Toshiro
APPLICANT: Tsukamoto, No. US20020099170Aliyo
APPLICANT: Tsukamoto, No. US20020099170Aliyo
APPLICANT: Tsukamoto, No. US20020099170Aliyo
APPLICANT: Yamasaki, Masatoshi
TITLE OF INVENTION: PROTEINS PROTEINS AND BLUE FLUORESCENT
TITLE OF INVENTION: PROTEINS
FILE REPERENCE: 046124-5005-05
CURRENT APPLICATION NUMBER: US/09/852,000
CURRENT APPLICATION NUMBER: US/09/852,000
PRIOR PRILING DATE: 1998-01-23
PRIOR PRILING DATE: 1998-01-23
PRIOR PRILING DATE: 1998-07-24
PRIOR PRILING DATE: 2000-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSKGEELFIGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.5%; Score 1234; DB 9; Length 238; Best Local Similarity 97.1%; Pred. No. 5.3e-124; Matches 231; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ), OTHER INFORMATION: Green fluorescent protein US-09-852-000-1
                                                                                                                                                                                                                         Sequence 1, Application US/09852000 Patent No. US20020099170A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Aequorea victoria FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-900-345A-125
                                                                                                                                                                               RESULT 14
US-09-852-000-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                g
                                                    ò
```

```
121 NRIELKGIDFKEDGNILGHKLEYNFISHNVYITADKOKNGIKANFKIRHNIEDGSVOLAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VITESXGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VITESYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDILV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPKEKRDHMVLLEFVTAAGITHGMDELYK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                 FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: GFP humanized
COTHER INFORMATION: control
US-09-900-345A-125
                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                         Length 238;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                       Score 1234; DB 10;
Pred. No. 5.3e-124;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: April 19, 2004, 15:13:19
Job time : 47 secs
                                                                                                                                                                                                                                                         Query Match 97.5%;
Best Local Similarity 97.1%;
Matches 231; Conservative
                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 185
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 125
LENGTH: 238
```

ö